

Run on: December 21, 2005, 13:54:50 ; Search time 8.35821 seconds

OM protein - protein search, using sw model

Title: US-10-717-138-2

Perfect score: 595

Sequence: 1 AYGIGLDITELKRKIASMAGR. SITHIKREYAAQVIERLSS 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 713107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_PEP:*

2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_PEP:*

3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PEP:*

4: /cgn2_6/ptodata/2/pubpaa/US109_NEW_PUB_PEP:*

5: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_PEP:*

6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB_PEP:*

7: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP:*

8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	159.5	26.8	125	US-10-467-657-7284
2	69	11.6	653	Sequence 7284, AP
3	65.5	11.0	653	Sequence 1286, AP
4	63.5	10.7	141	Sequence 3066, AP
5	63	10.6	607	Sequence 3184, AP
6	63	10.6	805	Sequence 77, AP1
7	62.5	10.5	308	Sequence 286, AP
8	62.5	10.5	525	Sequence 1316, AP
9	62	10.4	2725	Sequence 52, AP1
10	61.5	10.3	228	Sequence 2290, AP
11	61.5	10.3	240	Sequence 19, AP1
12	61.5	10.3	300	Sequence 1900, AP
13	60	10.1	217	Sequence 316, AP
14	60	10.1	327	Sequence 34, AP1
15	60	10.1	341	Sequence 8374, AP
16	60	10.1	691	Sequence 7170, AP
17	59	9.9	407	Sequence 1286, Application US/10821234
18	59	9.9	450	; Sequence 1286, Application US/10821234
19	59	9.9	548	; Publication No. US2005025514A1
20	59	9.9	567	; GENERAL INFORMATION:
21	59	9.9	599	; APPLICANT: Iabat, Ivan
22	59	9.9	650	; APPLICANT: Stache-Crain, Birgit
23	59	9.9	724	; APPLICANT: Andarmani, Susan
24	57.5	9.7	196	; APPLICANT: Tang, Y. Tom
25	57.5	9.7	709	; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

ALIGNMENTS

RESULT 1

US-10-467-657-7284

; Sequence 7284, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin9, version 1.04

; SEQ ID NO: 7284

; LENGTH: 125

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-7284

Query Match Best Local Similarity 26.8%; Score 159.5; DB 6; Length 125; Matches 42; Conservative 11; Mismatches 30; Indels 3; Gaps 2;

Qy	Db	Y
	3	YIGIGLDITELKRKIASMAGR-QKRFAERILITSELDQYELSEKRNKFPLGRAAKAFS
	3	YIGIGLDITELKRKIASMAGR-QKRFAERILITSELDQYELSEKRNKFPLGRAAKAFS
	61	KAFGTGIGRGSOFDIEBIRKONGKP 86
	61	KAVGTGIRGAWVSFCNIGIGHDALGKP 86

RESULT 2

US-10-821-234-1286

; Sequence 1286, Application US/10821234

; Sequence 1286, Application US/10821234

; Publication No. US2005025514A1

; GENERAL INFORMATION:

; APPLICANT: Iabat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

```

; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PILESEQ_Genes Version 1.0
; SEQ ID NO: 1286
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1-286

Query Match 11.6%; Score 69; DB 6; Length 653;
Best Local Similarity 33.8%; Pred. No. 5.1;
Matches 26; Conservative 12; Mismatches 31; Indels 8; Gaps 4;
QY 10 EUKRIS---MAGRKFRAEILTRSELDY-YELSEK-RKNEFLAGRFAA--KEAFSK 61
Db 536 EIERMONDAERKAEDKKLKERIDTRNELESIAYSUKNQIDKEKUGKLUSSEDKETMEK 595
QY 62 AFGTGIGRQLSFQDIEI 78
Db 596 AVEEKIEWLESHODADI 612

RESULT 3
US-10-467-657-694
; Sequence 694, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabettta
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO: 694
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

Query Match 10.7%; Score 63.5; DB 6; Length 141;
Best Local Similarity 27.6%; Pred. No. 2.9;
Matches 32; Conservative 22; Mismatches 31; Indels 31; Gaps 8;
QY 18 AGRKFRAEILTRSELDY-YELSEK-RKNEFLAGRFAA--SKA----- 62
Db 15 AAAQTWADTVFSCKPDDNNKYIEVKINNLVYSGFGRAKKETAIRNSKADLIGRSRW 74
QY 63 FGTGIGRQLSFQDIEBIRKDONGK-PYIICTKLSQAAVHSITHKEYAAQVIER 117
Db 75 QGMGSSGRATM----KONGEMFTWTGFD-----SVTHIE--SSGVVVER 115

RESULT 5
US-10-793-626-3184
; Sequence 3184, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3-80US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3184
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-10-793-626-3184

Query Match 10.6%; Score 63; DB 6; Length 567;
Best Local Similarity 29.9%; Pred. No. 19;
Matches 26; Conservative 15; Mismatches 36; Indels 10; Gaps 4;
QY 5 GLDITELKRKRIASMAGRO-KRRAEILTRSELDY--LSKRR----KNEF--LAGRF 53
Db 76 GLAV-ENERLAIQLQGOERKARAEYALERQIQRQVETDLERSQRTVDRDVQNDLSDVGNRF 134
QY 54 AKEAASKAFAFGIGRQLSF-QDIELRKDQNGKPYIICKS-SQAAVHVSHTHKEYAAQ 112
Db 135 AAE-----KQIAVYQKEKAERLRSQH--TEQEKQGGLAVEN--IRLATO 178
QY 113 VVTERLSS 120
Db 179 IEQERLIA 186

RESULT 4
US-10-467-657-3066
; Sequence 3066, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita

RESULT 6
US-10-927-641-77
; Sequence 77, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
; APPLICANT: Pereira, Ranjan
; APPLICANT: Rice, Stephen

```

APPLICANT: Eagleton, Clare
Applicant: Lasham, Annette
APPLICANT: Wood, Marion
APPLICANT: Visser, Elizabeth
TITLE OF INVENTION: Compositions and Methods for the
Title of Invention: Modification of Gene Expression
FILE REFERENCE: 11000_1036c4
CURRENT APPLICATION NUMBER: US/10/927,641
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/NZ00/00018
PRIOR FILING DATE: 2000-02-24
APPLICATION NUMBER: U.S. No. 60/146,591
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 143
SEQ ID NO: 77
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 805
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-10-927-641-77

RESULT 7
US-11-194-246-286
; Sequence 286, Application US/11194246
; Publication No. US20050272089A1
GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET

; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
FILE REFERENCE: 00592_051 (MER 268.05950101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2005-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 286
LENGTH: 308
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-286

Query Match 10.6%; Score 63; DB 6; Length 805;
Best Local Similarity 26.7%; Pred. No. 29; Mismatches 24; Indels 27; Gaps 4;
Matches 24; Conservative 17; Mismatches 27; Indels 22; Gaps 4;

QY 2 YIGGLDTTEKKIPLASMAAGRQPAERLITRSQDQYELSERKANEFLAGPAAKAFSK 61
Db 592 YGKNSKURELNUWVGGDRKDSDQESEMKKMVDLIEKYK--LNGQP----- 640

QY 62 AFGTGIGRQLSFDIEIRKDQNGKPY-TIC 90
Db 641 -----RWISSQMNRYR--NGELIYRIC 660

RESULT 7
US-11-194-246-286
; Sequence 286, Application US/11194246
; Publication No. US20050272089A1
GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET

; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
FILE REFERENCE: 00592_051 (MER 268.05950101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2005-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 286
LENGTH: 308
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-286

Query Match 10.5%; Score 62.5; DB 6; Length 525;
Best Local Similarity 26.8%; Pred. No. 19; Mismatches 26; Indels 13; Mismatches 31; Indels 27; Gaps 4;
Matches 26; Conservative 13; Mismatches 31; Indels 27; Gaps 4;

QY 19 GROKRPAERLITRSQDQYELSERKANEFLAGPAAKAFSKAROTGIGR 69
Db 49 GRIRYVSKI--GPELRQVFANDNEGPFRSDYTKNTIVLAGKYSR--MTSGTG-- 100

QY 70 QLSFQDIEIRKDQNGKPYTICLKUSQAVAVSITIK 106
Db 101 -----KDYEEGFYIQTWMFFLQATELHDWIE 127

RESULT 7
US-11-113-424-52
; Sequence 52, Application US/11113424
; Publication No. US20050260713A1
GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02

Query Match 10.5%; Score 62.5; DB 7; Length 308;
Best Local Similarity 27.1%; Pred. No. 9.9; Mismatches 19; Indels 23; Gaps 2;
Matches 19; Conservative 10; Mismatches 18; Indels 23; Gaps 2;

CURRENT APPLICATION NUMBER: US/11/005, 822
 CURRENT FILING DATE: 2005-02-11
 PRIOR APPLICATION NUMBER: 09/1606, 740
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: 60/141, 031
 PRIOR FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: 60/142, 101
 PRIOR FILING DATE: 1999-07-02
 PRIOR APPLICATION NUMBER: 60/148, 613
 PRIOR FILING DATE: 1999-08-12
 PRIOR APPLICATION NUMBER: 60/187, 970
 PRIOR FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: DE 19930476.9
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: DE 19931415.2
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931418.7
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931419.5
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931420.9
 PRIOR FILING DATE: 1999-07-08
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1158
 SEQ ID NO 316
 LENGTH: 217
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
 US-11-035-822-316

Query Match Best Local Similarity 31.2%; Score 60; DB 7; Length 217; Matches 30; Conservative 12; Mismatches 28; Indels 26; Gaps 6;

QY 34 LDQYELLS-EK-----RKHEFLRAFAERAKFSKAFGTVGRQLSFDQDIEIRKQO 82
 Db 24 LDIFHQLHLRALKVALVAHSVDIKAEGDARKCAGL-OHLGRSGD----PILRG 75

QY 83 NGKYIYIICTKUSQAVAHVSITHTKEYAAQVIERL 118
 Db 76 RGMP-----LWPSVSGSLTHBGFRAA-WPRL 104

RESULT 14
 US-10-67-657-34
 Sequence 34 Application US/10467657
 Publication No. US20050260581A1
 GENERAL INFORMATION:
 APPLICANT: CHIRON SPA
 APPLICANT: FONTANA Maria Rita
 APPLICANT: PIZZA Mariagrazia
 APPLICANT: MASIGNANI Vega
 APPLICANT: MONACI Elisabetta
 TITLE OF INVENTION: GONOCOCAL PROTEINS AND NUCLEIC ACIDS
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/467,657
 PRIOR FILING DATE: 2001-03-12
 NUMBER OF SEQ ID NOS: 9218
 SOFTWARE: SeqWin9, version 1.04
 SEQ ID NO 8374
 LENGTH: 341
 TYPE: PRT
 ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-8374

Query Match Best Local Similarity 24.5%; Score 60; DB 6; Length 341; Matches 36; Conservative 21; Mismatches 44; Indels 45; Gaps 7;

QY 12 KRIASHMAGRQRAERILTRSELDQYELSKRKE-----FLAGRFAAKERAKFSKAFGT 65
 Db 31 KRAAKESTROFRRAVKHQAGTVRNDR-NRLSARKSAKENIARMLSG--AKVSEDEALTC 86

QY 66 GIGRQSPDQEIRKQO-----NGKRYIIL-CTKLSQAV 98
 Db 87 GIMMRSLQDHYAQMELINFAEHTIVQVQRGLGLYCNTDDPANGESVLFACREASQVA 146

QY 99 RVSITHKEY-----AAAQVIERLSS 120
 Db 147 Q---WTKDFNDLSPNQRQVLRPLSN 169

Search completed: December 21, 2005, 14:13:52
 Job time : 9.35821 secs

Query Match Best Local Similarity 24.5%; Score 60; DB 6; Length 327; Matches 36; Conservative 21; Mismatches 44; Indels 46; Gaps 7;
 SEQ ID NO 34
 LENGTH: 327
 TYPE: PRT
 ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-34

QY . 66 GIGRQSPDQEIRKQO-----NGKRYIIL-CTKLSQAV 98
 Db 73 GIMMRSLQDHYAQMELINFAEHTIVQVQRGLGLYCNTDDPANGESVLFACREASQVA 132
 QY 99 RVSITHKEY-----AAAQVIERLSS 120
 Db 133 Q---WTKDFNDLSPNQRQVLRPLSN 155

Db 17 KRAAKESTROFRRAVKHQAGTVRNDR-NRLSARKSAKENIARMLSG--AKVSEDEALTC 72
 QY . 66 GIGRQSPDQEIRKQO-----NGKRYIIL-CTKLSQAV 98
 Db 73 GIMMRSLQDHYAQMELINFAEHTIVQVQRGLGLYCNTDDPANGESVLFACREASQVA 132

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:49:45 ; Search time 133.134 Seconds

(without alignments) 376.608 Million cell updates/sec

Title: US-10-717-138-2
Perfect score: 595
Sequence: 1 AYGIGLIDTELKRKIASMAGR..... SITHKEYAAQVIERLSS 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main: *
1: /cgn2_6/ptodata/1/pubpaal/us07_PUBCOMB.pep: *
2: /cgn2_6/ptodata/1/pubpaal/us08_PUBCOMB.pep: *
3: /cgn2_6/ptodata/1/pubpaal/us09_PUBCOMB.pep: *
4: /cgn2_6/ptodata/1/pubpaal/us10a_PUBCOMB.pep: *
5: /cgn2_6/ptodata/1/pubpaal/us10b_PUBCOMB.pep: *
6: /cgn2_6/ptodata/1/pubpaal/us11_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	595	100.0	120	3	US-09-770-834-2
2	595	100.0	120	4	US-10-717-138-2
3	591	99.3	121	3	US-09-771-383-1
4	591	99.3	121	3	US-09-770-834-12
5	591	99.3	121	4	US-10-717-138-12
6	591	99.3	119	4	US-10-282-122A-46229
7	51.1	51.1	119	4	US-10-282-122A-46229
8	287	48.2	118	4	US-10-282-122A-60496
9	281.5	47.3	124	4	US-10-282-122A-3855
10	279.5	47.0	117	4	US-10-282-122A-70857
11	278.5	46.8	119	4	US-10-282-122A-71569
12	278	46.7	119	3	US-09-771-383-5
13	278	46.7	119	3	US-09-770-834-5
14	278	46.7	119	4	US-10-717-138-6
15	277	46.6	119	3	US-09-815-242-5341
16	277	46.6	119	4	US-10-282-122A-44196
17	275	46.2	119	5	US-10-857-625-722
18	275	46.2	117	4	US-10-282-122A-57376
19	269	45.2	117	5	US-10-953-901-230
20	269	45.2	117	5	US-10-953-901-232
21	269	45.2	117	3	US-09-815-242-10776
22	267	44.9	117	4	US-10-282-122A-52394
23	262	44.0	117	5	US-10-501-282-74
24	250	42.0	113	5	US-10-501-282-72
25	244	41.0	120	4	US-10-282-122A-74124
26	243	40.8	120	5	US-10-472-928-3504
27	40.8				

ALIGNMENTS

RESULT 1
US-09-770-834-2
; Sequence 2, Application US/09770834
; Publication No. US20030211588A1
; GENERAL INFORMATION:
; APPLICANT: Parris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OR INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/09-770, 834
; CURRENT FILING DATE: 2001-10-12
; PRIORITY APPLICATION NUMBER: US 60/202, 466
; PRIORITY FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-770-834-2

Query Match 100.0%; Score 595; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.9e-63; Mismatches 0; Indels 0; Gaps 0;
Matches 120; Conservative 0; Mismatches 0;

QY 1 AYGIGLIDTELKRKIASMAGRKFRAEFLITSELDQYELSEKRKFRAEFLRAEAKFS 60
Db 1 AVGIGLIDTELKRKIASMAGRKFRAEFLITSELDQYELSEKRKFRAEFLRAEAKFS 60

61 KARGTGIGRQLSFDQDITRKDONGKPYIICKLKSQAHHVSTITHKEYAAQVIERLSS 120
61 KARGTGIGRQLSFDQDITRKDONGKPYIICKLKSQAHHVSTITHKEYAAQVIERLSS 120

RESULT 2
US-10-717-138-2
; Sequence 2, Application US/10717138
; Publication No. US20040078147A1
; GENERAL INFORMATION:
; APPLICANT: Parris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark

```

APPLICANT: Powers, Robert
APPLICANT: Xu, Guan-Yi
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
FILE REFERENCE: 2368/14
CURRENT APPLICATION NUMBER: US/10/717,138
CURRENT FILING DATE: 2003-11-19
PRIORITY APPLICATION NUMBER: US/09/770,834
PRIOR FILING DATE: 2001-10-12
PRIORITY APPLICATION NUMBER: US 60/202,466
PRIORITY FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 120
TYPE: PRT
ORGANISM: Bacillus subtilis
US-10-717-138-2

RESULT 3
Query Match          100.0%; Score 595; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.9e-63; Mismatches 0; Indels 0; Gaps 0;
Matches 120; Conservative 0; MisMatches 0; Index 0;
GENERAL INFORMATION:
Patent NO. US20020054562A1

Oy      1 AYGIGLDITELKRITASMACRQKPFRAERILTRSELQDYYELSEKRKNELFLAGRAEAKFS 60
Db      1 AYGIGLDITELKRITASMACRQKPFRAERILTRSELQDYYELSEKRKNELFLAGRAEAKFS 60
Oy      61 KAFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 120
Db      61 KAFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 120
Oy      62 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 120
Db      62 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 120
Db      63 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 120

US-09-771-383-1
Sequence 1, Application US/09771383
Patent NO. US20020054562A1

GENERAL INFORMATION:
APPLICANT: Parris, Kevin
APPLICANT: Somers, William
APPLICANT: Tam, Amy
APPLICANT: Lin, Laura
APPLICANT: Stahl, Mark
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
FILE REFERENCE: 2368/12
CURRENT APPLICATION NUMBER: US/09/771,383
CURRENT FILING DATE: 2001-01-25
PRIORITY APPLICATION NUMBER: US 60/178,639
PRIORITY FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 121
TYPE: PRT
ORGANISM: B. subtilis
US-09-771-383-1

Query Match          99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63; Mismatches 0; Indels 0; Gaps 0;
Matches 119; Conservative 0; MisMatches 0; Index 0;
GENERAL INFORMATION:
Patent NO. US20030211588A1

Oy      2 YGIGLDITELKRITASMACRQKPFRAERILTRSELQDYYELSEKRKNELFLAGRAEAKFS 61
Db      3 YGIGLDITELKRITASMACRQKPFRAERILTRSELQDYYELSEKRKNELFLAGRAEAKFS 62
Oy      62 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 120
Db      63 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 121
Oy      62 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 120
Db      63 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 121

RESULT 5
Query Match          99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63; Mismatches 0; Indels 0; Gaps 0;
Matches 119; Conservative 0; MisMatches 0; Index 0;
GENERAL INFORMATION:
APPLICANT: Parris, Kevin
APPLICANT: Somers, William
APPLICANT: Tam, Amy
APPLICANT: Lin, Laura
APPLICANT: Stahl, Mark
APPLICANT: Powers, Robert
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
FILE REFERENCE: 2368/14
CURRENT APPLICATION NUMBER: US/09/770,834
CURRENT FILING DATE: 2001-10-12
PRIORITY APPLICATION NUMBER: US 60/202,466
PRIORITY FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 121
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-770-834-12

Query Match          99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63; Mismatches 0; Indels 0; Gaps 0;
Matches 119; Conservative 0; MisMatches 0; Index 0;
GENERAL INFORMATION:
Patent NO. US20030211588A1

Oy      2 YGIGLDITELKRITASMACRQKPFRAERILTRSELQDYYELSEKRKNELFLAGRAEAKFS 61
Db      3 YGIGLDITELKRITASMACRQKPFRAERILTRSELQDYYELSEKRKNELFLAGRAEAKFS 62
Oy      62 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 120
Db      63 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 121
Oy      62 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 120
Db      63 AFGTGIGRQLSFDIERKDKONGKPYIICTKUSQAATHVSTHTKEYAAQVIERLSS 121

```

RESULT 6
US-10-717-138-12
; Sequence 12, Application US/10717138
; GENERAL INFORMATION:
; APPLICANT: Parris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-ri
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/10/717,138
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/770,834
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Bacillus sp.
; US-10-717-138-12

Query Match 99.3%; Score 591; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63; Mismatches 0; Indels 0; Gaps 0;
Matches 119; Conservative 0;

QY 2 KGIGLDTIELKRIASMAGRKRFAERLTREBDQYELSERKRNFLAGRFAKEAFSK 61
Db 3 VGTGLDTIELKRIASMAGRKRFAERLTREBDQYELSERKRNFLAGRFAKEAFSK 62

QY 62 AFGTGIGRQLSQDIEIRKDONGPKVICTKLQSQAATHVSTTHKEYAAQVWIERLS 120
Db 63 AFGTGIGRQLSQDIEIRKDONGPKVICTKLQSQAAVHVSITHKEYAAQVWIERLS 121

RESULT 7
US-10-282-122A-46229
; Sequence 46229, Application US/10282122A
; Publication No. US/0040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; FILE REFERENCE: ELITRA.034A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SEQ ID NO 46229
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Bacillus anthracis
; US-10-282-122A-46229

Query Match 51.1%; Score 304; DB 4; Length 119;
Best Local Similarity 54.2%; Pred. No. 2.3e-28; Mismatches 20; Indels 2; Gaps 1;
Matches 64; Conservative 20; Mismatches 32;

QY 3 GIGLDTIELKRIASMAGRKRFAERLTREBDQYELSERKRNFLAGRFAKEAFSK 62
Db 4 GIGIDTIELKRIEKMGLKFMERLTENERNVAKGLKGSRLTEFVAGRFAKEAFSK 63

QY 63 FGTGIGRQLSQDIEIRKDONGPKVICTKLQSQAHHVSITHKEYAAQVWIERLS 120
Db 64 VGTGIGKEVSFLDIEVRNDRGKPLITS--TEHTVHLSTSKEFAVAQVWIESSS 119

RESULT 8
US-10-282-122A-60496
; Sequence 60496, Application US/10282122A
; Publication No. US/0040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; FILE REFERENCE: ELITRA.034A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remind: Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 60496
 ; LENGTH: 118
 ; TYPE: PRT
 ; ORGANISM: Listeria monocytogenes
 ; US-10-282-122A-60496

 Query Match 48.2%; Score 287; DB 4; Length 118;
 Best Local Similarity 50.9%; Pred. No. 2.5e-26; Matches 58; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
 QY 3 GIGDUTELKRIASMAQRKQPAERLITRSELDQYELSEKRKNIFLAGRFRAEFSKA 62
 Db 4 GIGLONDILDKRQVVKVNEPKFTRIYERTEKEIKOQEYKRNKIEFLAFRAEAKA 63
 QY 63 FGTGIGRQLSQTDIRKDQNGKPYTICTKLSQAAYHVSITHKEYAAQWIE 116
 Db 64 NGTGFOKHLSTDVIELQVEDGRPHVTLPVKGGENVFVSITHTARSAAQWIE 117

 RESULT 9
 US-10-724-972A-3855
 ; Sequence 3855, Application US/1024972A
 ; Publication No. US20040147734A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Doucette-Stamm, Lynn
 ; APPLICANT: Bush, David
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: PATH03-15
 ; CURRENT APPLICATION NUMBER: US/10/724,972A
 ; CURRENT FILING DATE: 2003-12-01
 ; PRIOR APPLICATION NUMBER: 09/450,969
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: 09/134,001
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 7544
 ; SEQ ID NO: 3955
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: S. epidermidis
 ; US-10-724-972A-3855

 Query Match 47.3%; Score 281.5; DB 4; Length 124;
 Best Local Similarity 51.3%; Pred. No. 1.2e-25; Matches 61; Conservative 20; Mismatches 29; Indels 9; Gaps 4;
 QY 2 YGIGDUTELKRIASMAQRKQPAERLIT--RSELDQYELSEKRKNIFLAGRFRAEKA 58
 Db 10 YGIGDULIERIRIKNQ--NQKFVIELTTEERDKLNQ--TNEDRPLFLAGRTKEA 66
 QY 59 PSKAFGTGIGRQLSQTDIRKDQNGKPYTICTKLSQAAYHVSITHKEYAAQWIE 117
 Db 67 FSKALGTGIGKSVSFQDINCNDALGK--CIDIYPGFTVHSITHTENYAMSQVILEK 122

 RESULT 10
 US-10-282-122A-70857
 ; Sequence 70857, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Habelbeck, Robert
 ; APPLICANT: Olsene, Kari
 ; APPLICANT: Zoskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A

 Query Match 47.0%; Score 279.5; DB 4; Length 117;
 Best Local Similarity 51.3%; Pred. No. 2e-25; Matches 61; Conservative 19; Mismatches 30; Indels 9; Gaps 4;
 QY 2 YGIGDUTELKRIASMAQRKQPAERLIT--RSELDQYELSEKRKNIFLAGRFRAEKA 58
 Db 3 YGIGDULIERIRIKNQ-NQKFVIELTTEERDKLNQ--THEQRLPLFLAGRTKEA 59

 RESULT 11
 US-10-282-122A-71569
 ; Sequence 71569, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Habelbeck, Robert
 ; APPLICANT: Olsene, Kari
 ; APPLICANT: Zoskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIORITY APPLICATION NUMBER: 60/191,078
; PRIORITY FILING DATE: 2000-03-21
; PRIORITY APPLICATION NUMBER: 60/205,848
; PRIORITY FILING DATE: 2000-05-23
; PRIORITY FILING DATE: 2000-05-26
; PRIORITY APPLICATION NUMBER: 60/230,335
; PRIORITY APPLICATION NUMBER: 60/230,347
; PRIORITY FILING DATE: 2000-09-09
; PRIORITY APPLICATION NUMBER: 60/242,578
; PRIORITY FILING DATE: 2000-10-23
; PRIORITY APPLICATION NUMBER: 60/253,625
; PRIORITY FILING DATE: 2000-11-27
; PRIORITY APPLICATION NUMBER: 60/257,931
; PRIORITY FILING DATE: 2000-12-22
; PRIORITY APPLICATION NUMBER: 60/267,636
; PRIORITY FILING DATE: 2001-02-09
; PRIORITY APPLICATION NUMBER: 60/269,308
; SEQ ID NO: 71569
; LENGTH: 119
; TYPE: PRT
; ORGANISM: *Staphylococcus haemolyticus*
; US-10-282-122A-71569

Query Match 46.8%; Score 278.5; DB 4; Length 119;
; Best Local Similarity 50.0%; Pred. No. 2.7e-25; Matches 59; Conservative 22; Mismatches 32; Indels 5; Gaps 3;

Matches

Qy 2 YGIGDITEKLRIASMGROKRFAERILTSRBDQYEL-SEKRKNEFLAGRFAKEAF 59
; Db 3 HGIGDILEDRIDRKKAPEKOKLKVLTQEEQPHFSKREKRFGRFAKEAF 62

Qy 60 KAFGTGIGRQLSFDOTIEIRKDONGKPYIICTKLSQAVHVSITHKEYAAQVIER 117
; Db 63 SKALGTGIGKTVAFKDINCNDIKGP---CIDIYGFIVHVSISHTERYAMSQVLEK 117

RESULT 12
; Sequence 5, Application US/09711383
; Patent No. US20020034562A1

GENERAL INFORMATION:
; APPLICANT: Parris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
; TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
; FILE REFERENCE: 2268/12
; CURRENT APPLICATION NUMBER: US/09/771,383
; CURRENT FILING DATE: 2001-01-25
; PRIORITY APPLICATION NUMBER: US 60/178,639
; PRIORITY FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: *Staphylococcus*

US-09-771-383-5

RESULT 13
; US-09-770-834-6
; Sequence 6, Application US/09770834
; Publication No. US20030211588A1
; GENERAL INFORMATION:
; APPLICANT: Parris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; FILE REFERENCE: 2358/14
; CURRENT APPLICATION NUMBER: US/09/770,834
; CURRENT FILING DATE: 2001-10-12
; PRIORITY APPLICATION NUMBER: US 60/202,466
; PRIORITY FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: *Staphylococcus* sp.

US-09-770-834-6

Query Match 46.7%; Score 278; DB 3; Length 119;
; Best Local Similarity 48.7%; Pred. No. 3.1e-25; Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2;

Matches

Qy 2 YGIGDITEKLRIASMGROKRFAERILTSRBDQYEL-SEKRKNEFLAGRFAKEAF 60
; Db 3 HGIGDILEDRIDRKKAPEKOKLKVLTQEEQPHFSKREKRFGRFAKEAF 62

Qy 61 KAFGTGIGRQLSFDOTIEIRKDONGKPYIICTKLSQAVHVSITHKEYAAQVIER 117
; Db 63 KALGTGIGKTVAFKDINCNDIKGP---CIDIYGFIVHVSISHTERYAMSQVLEK 116

RESULT 14
; US-10-717-138-6
; Sequence 6, Application US/10717138
; Publication No. US2004007814A1
; GENERAL INFORMATION:
; APPLICANT: Parris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2268/14
; CURRENT APPLICATION NUMBER: US/10/717,138
; CURRENT FILING DATE: 2003-11-19
; PRIORITY APPLICATION NUMBER: US/09/770,834
; PRIORITY FILING DATE: 2001-10-12
; PRIORITY APPLICATION NUMBER: US 60/202,466
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 6

Query Match 46.7%; Score 278; DB 3; Length 119;
; Best Local Similarity 48.7%; Pred. No. 3.1e-25; Mismatches 31; Indels 4; Gaps 2;
; Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2;

```

; LENGTH: 119
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-10-717-138-6

Query Match 46.7%; Score 278; DB 4; Length 119;
Best Local Similarity 48.7%; Pred. No. 3.1e-25; Mismatches 31; Indels 4; Gaps 2;
Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2;

Qy 2 YGIGLDITELKRISAMGRQRFRAERILTRSDQYELS-EKRNKFPLAERFAEAFS 60
Db 3 HIGIVDLEIRNIDRQLQYKQPKLVERILTKHQHKFNFHQRKEFLAERFAEAFS 62

Qy 61 KAFGTGIGRQSFQDFEIRKONGKRYIICTKLSQAVHVSITHKEYAAQWVIER 117
Db 63 KALGTGIGKHAFNNDICYNDLGKPKI--DYEGETIVHVSISHTEHYAMSQVILEK 116

RESULT 15
US-03-815-242-5341
; Sequence 5341, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Faselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: E01RA_01IA
CURRENT APPLICATION NUMBER: US/03-815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/205,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: BlastSEQ for Windows Version 4.0
SEQ ID NO 5341
LENGTH: 119
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-03-815-242-5341

Query Match 46.6%; Score 277; DB 3; Length 119;
Best Local Similarity 48.7%; Pred. No. 4.1e-25; Mismatches 31; Indels 4; Gaps 2;
Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2;

Qy 2 YGIGLDITELKRISAMGRQRFRAERILTRSDQYELS-EKRNKFPLAERFAEAFS 60
Db 3 HIGIVDLEIRNIDRQLQYKQPKLVERILTKHQHKFNFHQRKEFLAERFAEAFS 62

Qy 61 KAFGTGIGRQSFQDFEIRKONGKRYIICTKLSQAVHVSITHKEYAAQWVIER 117
Db 63 KALGTGIGKHAFNNDICYNDLGKPKI--DYEGETIVHVSISHTEHYAMSQVILEK 116

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Search completed: December 21, 2005, 14:13:32
 Job time : 134.134 secs

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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:41:49 ; Search time 39.403 Seconds
 (without alignments)
 251.785 Million cell updates/sec

Title: US-10-717-138-2
 Perfect score: 595
 Sequence: 1 AYGIGLIDTELKRKIASMAGR.....SITHKEYAAQVIERLSS 120
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep: *
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep: *
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep: *
 6: /cgn2_6/ptodata/1/iaa/backfilesl.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB	ID	Description
1	595	100.0	120	2	US-09-770-834-2	Sequence 2, Appli
2	591	99.3	121	2	US-09-1670-846-4	Sequence 4, Appli
3	591	99.3	121	2	US-09-770-834-12	Sequence 12, Appli
4	591	99.3	121	2	US-09-771-383-1	Sequence 1, Appli
5	591	99.3	121	2	US-09-771-383-11	Sequence 10, Appli
6	283.5	47.3	124	2	US-09-134-01C-4274	Sequence 9, Appli
7	278	46.7	119	2	US-09-770-834-6	Sequence 13, Appli
8	278	46.7	119	2	US-09-771-383-5	Sequence 12, Appli
9	260	43.7	129	2	US-09-107-632A-6990	Sequence 11, Appli
10	243	40.8	120	2	US-09-583-10-3157	Sequence 2, Appli
11	243	40.8	122	2	US-09-987-144-2	Sequence 6, Appli
12	243	40.8	156	2	US-09-163-446-2	Sequence 5, Appli
13	243	40.8	157	2	US-09-107-433-4199	Sequence 3, Appli
14	203.5	35.2	138	2	US-09-543-61A-7596	Sequence 4, Appli
15	201.5	33.9	169	2	US-09-770-834-7	Sequence 7, Appli
16	201.5	33.9	169	2	US-09-771-383-6	Sequence 6, Appli
17	201	33.8	126	2	US-09-771-383-8	Sequence 8, Appli
18	189.5	31.8	125	2	US-09-728-742A-10	Sequence 10, Appli
19	189.5	31.8	126	2	US-09-770-834-8	Sequence 9, Appli
20	189.5	31.8	126	2	US-09-771-383-7	Sequence 7, Appli
21	189.5	31.8	159	2	US-09-489-039A-11671	Sequence 11, Appli
22	189.5	31.8	122	2	US-09-198-52A-330	Sequence 3, Appli
23	177.5	29.8	122	2	US-09-770-834-4	Sequence 4, Appli
24	177.5	29.8	122	2	US-09-771-383-3	Sequence 5, Appli
25	177.5	29.8	122	2	US-09-771-383-3	Sequence 6, Appli
26	177.5	29.8	133	2	US-09-438-185A-315	Sequence 7, Appli
27	177.5	29.1	125	2	US-09-770-834-11	Sequence 11, Appli

RESULT 2
 US-09-163-446-4
 ; Sequence 4, Application US/09163446
 ; Patent No. 6515119
 ; GENERAL INFORMATION:
 ; APPLICANT: Fritz Christian
 ; APPLICANT: Youngman, Philip
 ; APPLICANT: Guzman, Luz Maria
 ; TITLE OF INVENTION: USE OF S-YDCB AND B-YPCB, ESSENTIAL BACTERIAL GENES
 ; FILE REFERENCE: 07334/097001

CURRENT APPLICATION NUMBER: US/09/163,446
 CURRENT FILING DATE: 1998-09-30
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 4
 LENGTH: 121
 TYPE: PRT
 ORGANISM: Streptococcus pneumoniae
 US-09-163-446-4

Query Match 99.3%; Score 591; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.5e-63; Mismatches 0; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGLDITELKRKIASMAGRKPAERILTRSELQYELSEKRKNELLAGRFAKEAFSK 61
 Db 3 YGIGLDITELKRKIASMAGRKPAERILTRSELQYELSEKRKNELLAGRFAKEAFSK 62

QY 62 AFGTGIGRQLSFDQIEIRKDQNGPKYIICTKLSQAHHVSIITHKEYAAQVIERLSS 120
 Db 63 AFGTGIGRQLSFDQIEIRKDQNGPKYIICTKLSQAHHVSIITHKEYAAQVIERLSS 121

RESULT 3
 US-09-770-834-12
 Sequence 12, Application US/09770834
 Patent No. 6564162

GENERAL INFORMATION:

APPLICANT: Parris, Kevin
 APPLICANT: Somers, William
 APPLICANT: Tam, Amy
 APPLICANT: Lin, Laura
 APPLICANT: Stahl, Mark
 APPLICANT: Powers, Robert
 APPLICANT: Xu, Guan-Yi
 TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
 TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
 FILE REFERENCE: 2368/14
 CURRENT APPLICATION NUMBER: US/09/770, 834
 CURRENT FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: US 60/202, 466
 PRIOR FILING DATE: 2000-05-08
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 12
 LENGTH: 121
 TYPE: PRT
 ORGANISM: Bacillus sp.
 US-09-770-834-12

Query Match 99.3%; Score 591; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.5e-63; Mismatches 0; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGLDITELKRKIASMAGRKPAERILTRSELQYELSEKRKNELLAGRFAKEAFSK 61
 Db 3 YGIGLDITELKRKIASMAGRKPAERILTRSELQYELSEKRKNELLAGRFAKEAFSK 62

QY 62 AFGTGIGRQLSFDQIEIRKDQNGPKYIICTKLSQAHHVSIITHKEYAAQVIERLSS 120
 Db 63 AFGTGIGRQLSFDQIEIRKDQNGPKYIICTKLSQAHHVSIITHKEYAAQVIERLSS 121

RESULT 4
 US-09-771-383-1
 Sequence 1, Application US/09771383
 Patent No. 6557150

GENERAL INFORMATION:

APPLICANT: Parris, Kevin
 APPLICANT: Somers, William
 APPLICANT: Tam, Amy
 APPLICANT: Lin, Laura
 APPLICANT: Stahl, Mark

TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
 FILE REFERENCE: 2369/12
 CURRENT APPLICATION NUMBER: US/09/771, 383
 CURRENT FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: US 60/178, 639
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 11
 LENGTH: 121
 TYPE: PRT
 ORGANISM: Bacillus
 US-09-771-383-1

Query Match 99.3%; Score 591; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.5e-63; Mismatches 0; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGLDITELKRKIASMAGRKPAERILTRSELQYELSEKRKNELLAGRFAKEAFSK 61
 Db 3 YGIGLDITELKRKIASMAGRKPAERILTRSELQYELSEKRKNELLAGRFAKEAFSK 62

QY 62 AFGTGIGRQLSFDQIEIRKDQNGPKYIICTKLSQAHHVSIITHKEYAAQVIERLSS 120
 Db 63 AFGTGIGRQLSFDQIEIRKDQNGPKYIICTKLSQAHHVSIITHKEYAAQVIERLSS 121

RESULT 5
 US-09-771-383-11
 Sequence 11, Application US/09771383
 Patent No. 6557150

GENERAL INFORMATION:

APPLICANT: Parris, Kevin
 APPLICANT: Somers, William
 APPLICANT: Tam, Amy
 APPLICANT: Lin, Laura
 APPLICANT: Stahl, Mark

TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
 TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
 FILE REFERENCE: 2368/12
 CURRENT APPLICATION NUMBER: US/09/771, 383
 CURRENT FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: US 60/178, 639
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 11
 LENGTH: 121
 TYPE: PRT
 ORGANISM: Bacillus
 US-09-771-383-11

Query Match 99.3%; Score 591; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2.5e-63; Mismatches 0; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGLDITELKRKIASMAGRKPAERILTRSELQYELSEKRKNELLAGRFAKEAFSK 61
 Db 3 YGIGLDITELKRKIASMAGRKPAERILTRSELQYELSEKRKNELLAGRFAKEAFSK 62

QY 62 AFGTGIGRQLSFDQIEIRKDQNGPKYIICTKLSQAHHVSIITHKEYAAQVIERLSS 120
 Db 63 AFGTGIGRQLSFDQIEIRKDQNGPKYIICTKLSQAHHVSIITHKEYAAQVIERLSS 121

RESULT 6
 US-09-134-001C-4274
 Sequence 4274, Application US/09134001C
 Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

Page 3

TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134, 001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064, 964
 PRIOR FILING DATE: 1997-11-08
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO: 4274
 LENGTH: 124
 TYPE: PRT
 ORGANISM: *Staphylococcus epidermidis*
 US-09-134-001C-4274

 Query Match 47.3%; Score 281.5; DB 2; Length 124;
 Best Local Similarity 51.3%; Pred. No. 4.4e-26;
 Matches 61; Conservative 20; Mismatches 29; Indels 9; Gaps 4;
 ; Sequence 6, Application US/09770834
 ; Patent No. 6684162
 GENERAL INFORMATION:
 ; APPLICANT: Parris, Kevin
 ; APPLICANT: Somers, William
 ; APPLICANT: Tam, Amy
 ; APPLICANT: Lin, Laura
 ; APPLICANT: Stahl, Mark
 ; APPLICANT: Powers, Robert
 ; APPLICANT: Xu, Guan-Yi
 TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
 TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
 FILE REFERENCE: 2368/14
 CURRENT APPLICATION NUMBER: US/09/770, 834
 CURRENT FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: US 60/202, 466
 PRIOR FILING DATE: 2000-05-08
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 6
 LENGTH: 119
 TYPE: PRT
 ORGANISM: *Staphylococcus*
 US-09-770-834-6

 Query Match 46.7%; Score 278; DB 2; Length 119;
 Best Local Similarity 48.7%; Pred. No. 1.1e-25;
 Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2;
 ; Sequence 6, Application US/09770834
 ; Patent No. 6684162
 GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTRICOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107, 532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085, 598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinille, Pamela Deneke
 REGISTRATION NUMBER: 40, 489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 6990:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 129 amino acids
 TYPE: amino acid

RESULT 8
 US-09-771-383-5
 ; Sequence 6, Application US/09771383
 ; Patent No. 6957150
 ; GENERAL INFORMATION:

TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: yes
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1...129
 SEQUENCE DESCRIPTION: SEQ ID NO: 6990:
 US-09-107-532A-6990

Query Match 43.7%; Score 260; DB 2; Length 129;
 Best Local Similarity 48.2%; Pred. No. 1.8e-23; Mismatches 55; Conservative 22; Gaps 2; Indels 2; Gaps 2; Matches 55; Conservative 22; Mismatches 35; Indels 2; Gaps 2;

QY 3 GIGIDITELKRITASMGAGRKAERIILRSLSQDQYELSERGEKRNELAGRRAKEAFSKA 62
 Db 17 GIGIDIAVELPRTLIEKKPKTARILTSMDNLKFLQSLPFRQVPLGGRWAKAFSKA 76

QY 63 FGTGIGRQLSFQDIEIRKDQNGKPYIICTKLSSQAQVHSITHTKEYAAQVIE 116
 Db 77 MGTGIGK-VTFQDVEILKNENQ-P-WTRSPHEGNWNSITHNETAFAQIILE 128

RESULT 10
 US-00-583-110-3157 Application US/09583110
 ; Sequence 3157, Application US/09583110
 ; Patent No. 6599703
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al.
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 ; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
 ; FILE REFERENCE: PATHO-07A
 ; CURRENT APPLICATION NUMBER: US/09/583,110
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/107,433
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/085,131
 ; PRIOR FILING DATE: 1998-05-12
 ; PRIOR APPLICATION NUMBER: US 60/051,553
 ; PRIOR FILING DATE: 1997-07-02
 ; SEQ ID NO 3157
 ; LENGTH: 120
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-03-583-110-3157

Query Match 40.8%; Score 243; DB 2; Length 120;
 Best Local Similarity 44.1%; Pred. No. 1.8e-21; Mismatches 52; Conservative 25; Gaps 3; Indels 10; Gaps 3; Matches 52; Conservative 25; Mismatches 31; Indels 10; Gaps 3;

QY 3 GIGIDITELKRITASMGAGRKAERIILRSLSQDQYELSERGEKRNELAGRRAKEAFSKA 62
 Db 6 GHGIDIELASIESAVTRHFGAFRKVLTQEMERFTSKGRRQEVLAGRWSAKEAFSKA 65

QY 63 FGTGIGRQLSFQDIEIRKDQNGKPYIICTKLSSQA---AVHSITHTKEYAAQVIE 116
 Db 66 MGTGISK-LGFQDIEVLNNERGAPY---FSQAPPSGKWIWLISHTDQFVTASVILLE 117

RESULT 11
 US-00-987-144-2 Application US/09163446
 ; Sequence 2, Application US/09163446
 ; Patent No. 6515119
 ; GENERAL INFORMATION:
 ; APPLICANT: Fritz, Christian
 ; APPLICANT: Youngman, Philip
 ; APPLICANT: Guzman, Luz-Maria
 ; TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
 ; FILE REFERENCE: 07334/097001
 ; CURRENT APPLICATION NUMBER: US/09/163,446
 ; CURRENT FILING DATE: 1998-09-30
 ; NUMBER OF SEQ ID NO: 12
 ; NUMBER OF SEQ ID NO: 12
 ; SEQ ID NO 2
 ; LENGTH: 156
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-09-163-446-2

Query Match 40.8%; Score 243; DB 2; Length 156;
 Best Local Similarity 44.1%; Pred. No. 2.6e-21; Mismatches 52; Conservative 25; Gaps 3; Indels 10; Gaps 3; Matches 52; Conservative 25; Mismatches 31; Indels 10; Gaps 3;

QY 3 GIGIDITELKRITASMGAGRKAERIILRSLSQDQYELSERGEKRNELAGRRAKEAFSKA 62
 Db 40 GHGIDIEELASIESAVTRHFGAFRKVLTQEMERFTSKGRRQEVLAGRWSAKEAFSKA 99

QY 63 FGTGIGRQLSFQDIEIRKDQNGKPYIICTKLSSQA---AVHSITHTKEYAAQVIE 116
 Db 100 MGTGISK-LGFQDIEVLNNERGAPY---FSQAPPSGKWIWLISHTDQFVTASVILLE 115

RESULT 12
 US-09-163-446-2
 ; Sequence 2, Application US/09163446
 ; Patent No. 6515119
 ; GENERAL INFORMATION:
 ; APPLICANT: Fritz, Christian
 ; APPLICANT: Youngman, Philip
 ; APPLICANT: Guzman, Luz-Maria
 ; TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
 ; FILE REFERENCE: 07334/097001
 ; CURRENT APPLICATION NUMBER: US/09/163,446
 ; CURRENT FILING DATE: 1998-09-30
 ; NUMBER OF SEQ ID NO: 12
 ; NUMBER OF SEQ ID NO: 12
 ; SEQ ID NO 2
 ; LENGTH: 156
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-09-163-446-2

Query Match 40.8%; Score 243; DB 2; Length 156;
 Best Local Similarity 44.1%; Pred. No. 2.6e-21; Mismatches 52; Conservative 25; Gaps 3; Indels 10; Gaps 3; Matches 52; Conservative 25; Mismatches 31; Indels 10; Gaps 3;

QY 3 GIGIDITELKRITASMGAGRKAERIILRSLSQDQYELSERGEKRNELAGRRAKEAFSKA 62
 Db 40 GHGIDIEELASIESAVTRHFGAFRKVLTQEMERFTSKGRRQEVLAGRWSAKEAFSKA 99

QY 63 FGTGIGRQLSFQDIEIRKDQNGKPYIICTKLSSQA---AVHSITHTKEYAAQVIE 116
 Db 100 MGTGISK-LGFQDIEVLNNERGAPY---FSQAPPSGKWIWLISHTDQFVTASVILLE 115

RESULT 13
 US-00-987-144-2 Application US/09163446
 ; Sequence 2, Application US/09163446
 ; Patent No. 6515119
 ; GENERAL INFORMATION:
 ; APPLICANT: Roseck Jr., Paul R.
 ; TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Eli Lilly and Company
 ; STREET: Lilly Corporate Center

RESULT 13 US-09-107-433-4199
 Sequence 4199, Application US/09107433
 Patent No. 6800744
 GENERAL INFORMATION:
 APPLICANT: Lynn A. Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 5,406
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: <Unknown>
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: <Unknown>
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,433
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/ 085131
 FILING DATE: May 12, 1998
 APPLICATION NUMBER: 60/051553
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arniello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 893-5007
 TELEFAX: (781) 893-8277
 INFORMATION FOR SEQ ID NO: 4199:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 157 amino acids
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORGANISM: Streptococcus pneumoniae
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1...157
 SEQUENCE DESCRIPTION: SEQ ID NO: 4199:
 ; US-09-107-433-4199
 Query Match 40.8%; Score 243; DB 2; Length 157;
 Best Local Similarity 41.1%; Pred. No. 2.6e-21; Mismatches 52; Conservative 25; MisMatches 31; Indels 10; Gaps 3;
 Matches 52; Conservative 25; MisMatches 31; Indels 10; Gaps 3;
 QY 3 GIGIDITELKRIASMAQRKRAERILRSELDQYELSEKRKNFLAGRPAKEAFSKA 62
 41 GHGIDIEELASIESAVTRHFGFAKEVLTQAEQEMERTFLKGRROFLYLAGRWSAKEAFSKA 100
 QY 63 FGTGIGRQLSFQDIDIRKDKONGKPVIICKLSSQA---AVHVSITHTKEYAAQWIE 116
 101 MTGIGSK-LGFQDLEVNNGRGPY---FSQAPFSKGWLSTHSHTQFVTASVIE 152
 RESULT 14 US-09-543-681A-7596
 Sequence 7596, Application US/09543681A
 Patent No. 6605749
 GENERAL INFORMATION:
 APPLICANT: GARY BRETON
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709_1002-001
 CURRENT APPLICATION NUMBER: US/09/543, 681A
 CURRENT FILING DATE: 2000-04-05
 PRIOR APPLICATION NUMBER: US 60/1128, 706
 PRIOR FILING DATE: 1999-04-09
 NUMBER OF SEQ ID NOS: 8344
 SEQ ID NO 7596
 LENGTH: 158
 TYPE: PRT
 ORGANISM: Proteus mirabilis
 US-09-543-681A-7596
 Query Match 35.2%; Score 209.5; DB 2; Length 138;
 Best Local Similarity 41.1%; Pred. No. 2.3e-17; Mismatches 40; Indels 11; Gaps 4;
 Matches 51; Conservative 22; MisMatches 74
 QY 3 GIGIDITELKRIASMAQRKRAERILRSELDQYELSEKRKNFLAGRPAKEAFSK 61
 Db 17 GGMGDIVEISRREEELIGRSGRRLRLLTQNHWIYQ-SHKOVPFLAKRFAVKA 74
 QY 62 ARGTGIGROLSPQDIETRKDQNGKPYI---ICTKLSQQA---AVHVSITHTKEYAAQV 113
 Db 75 ALGTGIGRIGLAPNHFEVANDELGKPTLHFLAWAKEMAQKAGINNAHVTLADQBRYACATV 134
 QY 114 VIER 117
 Db 135 ILLK 138
 RESULT 15 US-09-770-834-7
 Sequence 7, Application US/09770834
 Patent No. 6624162
 GENERAL INFORMATION:
 APPLICANT: Pariss, Kevin
 APPLICANT: Somers, William
 APPLICANT: Tam, Amy
 APPLICANT: Lin, Laura
 APPLICANT: Stahl, Marc
 APPLICANT: Powers, Robert
 APPLICANT: Xu, Guan-Yi
 APPLICANT: Cao, Yan
 TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE FILE REFERENCE: 2368/14
 CURRENT APPLICATION NUMBER: US/09/770, 834
 CURRENT FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: US 60/202, 466
 PRIOR FILING DATE: 2000-05-08
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 7
 LENGTH: 169
 TYPE: PRT
 ORGANISM: Thermotoga sp.
 US-09-770-834-7
 Query Match 33.9%; Score 201.5; DB 2; Length 169;
 Best Local Similarity 42.4%; Pred. No. 2.8e-16; Mismatches 50; Conservative 23; MisMatches 30; Indels 15; Gaps 7;
 Matches 50; Conservative 23; MisMatches 30; Indels 15; Gaps 7;
 QY 3 GIGIDITELKRIASMAQRKRAERILRSELDQYELSEKRKNFLAGRPAKEAFSKA 62
 4 GVGIDIVLVERV---PEKAFBRLGESEKRLF--LTKRKREFAGRFALKEAFFKA 55
 QY 63 FGTGIGRQLSFQDIDIRKDKONGKPVIICKLSSQA---AVHVSITHTKEYAAQWIE 117
 Db 56 LGTGLNGLH-SFTVEP-LESNGRP-VLUVHKPFGFENYAHVSLHDR-FAVALVWIK 109
 Search completed: December 21, 2005, 13:55:50
 Job time : 40.403 secs

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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:41:34 ; Search time 174.925 Seconds
(without alignments)
483.997 Million cell updates/sec

Title: US-10-717-138-2

Perfect score: 595
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Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
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2: uniprot_trembl:
[1]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	591	99.3	121	1 ACPS_BACSU
2	334.5	56.2	129	1 ACPS_GEOKA
3	329.5	55.4	117	1 ACPS_BASCK
4	313	52.6	119	1 ACPS_BACIL
5	304	51.1	119	1 ACPS_BACAN
6	304	51.1	119	1 ACPS_BACII
7	303	50.9	119	2 Q4MPT7_BACCE
8	300	50.9	119	1 ACPS_BACZ
9	297	49.9	119	1 ACPS_BACHD
10	287	48.2	118	1 ACPS_LISME
11	287	48.2	118	1 ACPS_LISMO
12	283	47.6	118	1 ACPS_LISTIN
13	279.5	47.0	117	1 ACPS_STAEP
14	279.5	47.0	117	1 ACPS_STABO
15	278.5	46.8	119	2 Q4LVG_STAHJ
16	278	46.7	119	1 ACPS_STAAC
17	278	46.7	119	1 ACPS_STAAU
18	277.5	46.6	119	1 ACPS_OCEH
19	277	46.2	119	1 ACPS_STAAM
20	275	46.2	119	1 ACPS_STAAR
21	275	46.2	119	1 ACPS_STAAR
22	275	46.2	119	1 ACPS_STAAS
23	275	46.2	119	1 ACPS_STAAU
24	275	46.2	119	1 ACPS_STAAU
25	275	45.2	119	1 ACPS_ENTPA
26	261	43.9	119	1 ACPS_LACIA
27	252.5	42.4	120	1 ACPS_LACPL
28	245	41.4	119	1 ACPS_LACRE
29	245	41.2	117	1 ACPS_LACRE
30	243	40.8	120	1 ACPS_STREN
31	243	40.8	120	1 ACPS_STRR6

RESULT 1	ACPS_BACSU	STANDARD:	PRT:	121 AA.
ID	P96618;			
AC				
DT	30-MAY-2000	(Rel. 39, Created)		
DT	30-MAY-2000	(Rel. 39, last sequence update)		
DT	13-SEP-2005	(Rel. 48, last annotation update)		
DE	Holo-acyl-carrier-protein synthase (EC 2.7.8.7) (Holo-ACP synthase) (4'-Phosphopantetheinyl transferase acps).			
GN	Name-acps: OrderedlocusNames=BSU04620;			
OS	Bacillus subtilis			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OU				
RN				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=168;			
RC	MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;			
RA	Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G., Alvedro V., Bessieres P., Boletin A., Borchart S., Borriss R., Bourquier L., Brans A., Braun M., Brignall S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Duesternooft A., Enrich S.D., Emmerson P.T., Entian K.-D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Fujita Y., Furia S., Galizzi A., Galleron N., Ghim S.-Y., Glaser P., Goiffon A., Golightly B.J., Grandi G., Guiseppi G., Guy B.-J., Haga K., Hatch J., Harwood C.R., Henaut A., Hilbert H., Hollappel S., Hosono S., Hullio M.-F., Itaya M., Jones L.-M., Joris B., Karamoto D., Kasahara Y., Klaerz-Blanchard M., Klein C., Kobayashi Y., Koetteler P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarovic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C., Medina C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogihara A., Outegia B., Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Puig P., Purnelle B., Rapoport G., Ray M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Seiguchi J., Sekowska A., Seror S.J., Sevor P., Shin B.-S., Soldo B., Sorokin A., Tacconi B., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandembol M., Vannier F., Vassarotti A., Viari A., Wambert R., Wedler B., Wedler H., Weitzsaegeger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshioka H.-F., Zumstein E., Yoshikawa H., Danchin A.,			
RA	The complete genome sequence of the Gram-positive bacterium Bacillus			

053318 vibrio fisc
091pb6 vibrio chol
084c72 vibrio vuln
07mhp2 vibrio vuln
05fmh3 lactobacill
P63471 streptococc
P63472 streptococc
Q86f3 streptococc
Q5ly70 streptococc
Q5m2s6 streptococc
Q871p3 vibrio para
Q91ir5 clostridium
P63473 streptococc
Q5kxa3 streptococc

ALIGNMENTS

RESULT 1	ACPS_BACSU	STANDARD:	PRT:	121 AA.
ID	P96618;			
AC				
DT	30-MAY-2000	(Rel. 39, Created)		
DT	30-MAY-2000	(Rel. 39, last sequence update)		
DT	13-SEP-2005	(Rel. 48, last annotation update)		
DE	Holo-acyl-carrier-protein synthase (EC 2.7.8.7) (Holo-ACP synthase) (4'-Phosphopantetheinyl transferase acps).			
GN	Name-acps: OrderedlocusNames=BSU04620;			
OS	Bacillus subtilis genome;"			
OC	Bacillus subtilis			
OU				
RN				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=168;			
RC	MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;			
RA	Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G., Alvedro V., Bessieres P., Boletin A., Borchart S., Borriss R., Bourquier L., Brans A., Braun M., Brignall S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Duesternooft A., Enrich S.D., Emmerson P.T., Entian K.-D., Errington J., Fabret C., Ferrari E., Fouger D., Fritz C., Fujita M., Fujita Y., Furia S., Galizzi A., Galleron N., Ghim S.-Y., Glaser P., Goiffon A., Golightly B.J., Grandi G., Guiseppi G., Guy B.-J., Haga K., Hatch J., Harwood C.R., Henaut A., Hilbert H., Hollappel S., Hosono S., Hullio M.-F., Itaya M., Jones L.-M., Joris B., Karamoto D., Kasahara Y., Klaerz-Blanchard M., Klein C., Kobayashi Y., Koetteler P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarovic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C., Medina C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogihara A., Outegia B., Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Puig P., Purnelle B., Rapoport G., Ray M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Seiguchi J., Sekowska A., Seror S.J., Sevor P., Shin B.-S., Soldo B., Sorokin A., Tacconi B., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandembol M., Vannier F., Vassarotti A., Viari A., Wambert R., Wedler B., Wedler H., Weitzsaegeger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshioka H.-F., Zumstein E., Yoshikawa H., Danchin A.,			
RA	The complete genome sequence of the Gram-positive bacterium Bacillus			

"The complete genome sequence of the Gram-positive bacterium Bacillus

Query Match Similarity 51.1%; Score 304; DB 1; Length 119;
 Best Local Similarity 54.2%; Pred. No. 2.2e-20; Mismatches 32; Indels 2; Gaps 1;

Matches 64; Conservative 20; MisMatches 32; Del 1; Insert 1;

QY 3 GIGLDITELKLTASMGROKPFRAERILTRSEEDOYELSERKRNFLAGRAKEAFSKA 62
 4 GIGIDIELNRIEMLDKLKEMERILTENERNVAKLGKGSRLTEVAGRAKEAFSKA 63

Db 63 FGTGIGQLSFDIETRKDQKPYIICTKLSQAVHVSITHKEYAAQVIERLS 119
 64 VGTGIGKEVSLDEVRNDRGKPLITS--TEHVHSISHSKEFAVAQVWLESS 118

RESULT 7

ACPS_BACC1 ID ACPS_BACCI STANDARD; PRT; 119 AA.

AC Q73ET8; ID 04MPFT7; 10-MAY-2005 (Rel. 47, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Holo-(Acyl-carrier protein) synthase (EC 2.7.8.7) (holo-ACP synthase)
 4'-phosphopantetheinyl transferase acps).

DE Name-acps; OrderedLocusNames=BCE0270;

GN Bacillus cereus (strain ATCC 10987);
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=269801;

OX NCBI_TaxID=22523;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PUBMED=14960714; DOI=10.1093/nar/gkn258;

RX Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.B., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Klotsteck A.B., Fraser C.M., Read T.D., RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic adaptations and a large plasmid related to *Bacillus anthracis* pXO1."; RT Rasko D.A., Ravel J., Chapman G.D., Chute M.D., Hoffmaster A.R., De B.K., Sacki C.T., FitzGerald C., Mayer L.W., Maistro C.K., Barker M., Jiang L., Cer R.Z., Read T.D., RT Popovic T., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D., RR STRAIN=G9241;

RX PubMed=15155910; DOI=10.1073/pnas.0402414101;

RX Rasko D.A., Ravel J., Rasko D.A., Hoffman A.R., De B.K., Sacki C.T., FitzGerald C., Mayer L.W., Maistro C.K., Barker M., Jiang L., Cer R.Z., Read T.D., RR Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D., RR "Identification of anthrax toxin genes in a *Bacillus cereus* associated with an illness resembling inhalation anthrax"; RT Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454 (2004).

RX DR -!- CAUTION: The sequence shown here is derived from an ENBL/GenBank/DBJ whole genome shotgun (WGS) entry which is CC preliminary data.

RX DR EMBL; AAEK0100017; BALI4228.1; -; Genomic_DNA.

RX KW Transferase; 119 AA; 13142 MW; OBE16DAB95812BDB CRC64;

SQ SEQUENCE

Query Match Similarity 50.9%; Score 303; DB 2; Length 119;
 Best Local Similarity 54.7%; Pred. No. 2.7e-20; Mismatches 32; Indels 2; Gaps 1;

Matches 64; Conservative 19; MisMatches 32; Del 1; Insert 1;

QY 3 GIGLDITELKLTASMGROKPFRAERILTRSEEDOYELSERKRNFLAGRAKEAFSKA 62
 4 GIGIDIELNRIEMLDKLKEMERILTENERNVAKLGKGSRLTEVAGRAKEAFSKA 63

Db 63 FGTGIGQLSFDIETRKDQKPYIICTKLSQAVHVSITHKEYAAQVIERLS 119
 64 VGTGIGKEVSLDEVRNDRGKPLITS--TEHVHSISHSKEFAVAQVWLESS 118

RESULT 8

Q4MPFT7_BACCE ID 04MPFT7; 13-SEP-2005 (TREMBurel. 31, Last sequence update)

AC Q4MPFT7; 13-SEP-2005 (TREMBurel. 31, Last annotation update)

DE Holo-(Acyl-carrier protein) synthase (EC 2.7.8.7).
 Name-acps; ORName=BCE_G9241_0240;

GN Bacillus cereus G9241;

OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=269801;

OX NCBI_TaxID=22523;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX STRAIN=G9241;

RX PubMed=15155910; DOI=10.1073/pnas.0402414101;

RX Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D., Maistro C.K., De B.K., Sacki C.T., FitzGerald C., Mayer L.W., Maistro C.K., Barker M., Jiang L., Cer R.Z., Read T.D., RR Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D., RR "Identification of anthrax toxin genes in a *Bacillus cereus* associated with an illness resembling inhalation anthrax"; RT Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454 (2004).

RX DR -!- CAUTION: The sequence shown here is derived from an ENBL/GenBank/DBJ whole genome shotgun (WGS) entry which is CC preliminary data.

RX DR EMBL; AAEK0100017; BALI4228.1; -; Genomic_DNA.

RX KW Transferase; 119 AA; 13142 MW; OBE16DAB95812BDB CRC64;

SQ SEQUENCE

Query Match Similarity 50.9%; Score 303; DB 2; Length 119;
 Best Local Similarity 54.7%; Pred. No. 2.7e-20; Mismatches 32; Indels 2; Gaps 1;

Matches 64; Conservative 19; MisMatches 32; Del 1; Insert 1;

QY 3 GIGLDITELKLTASMGROKPFRAERILTRSEEDOYELSERKRNFLAGRAKEAFSKA 62
 4 GIGIDIELNRIEMLDKLKEMERILTENERNVAKLGKGSRLTEVAGRAKEAFSKA 63

Db 63 FGTGIGQLSFDIETRKDQKPYIICTKLSQAVHVSITHKEYAAQVIERLS 119
 64 VGTGIGKEVSLDEVRNDRGKPLITS--TEHVHSISHSKEFAVAQVWLESS 118

RESULT 9

ACPS_BACC2 ID ACPS_BACCZ STANDARD; PRT; 119 AA.

AC 063GX2; ID 04MPFT7; 10-MAY-2005 (Rel. 47, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE 13-SEP-2005 (Rel. 48, Last annotation update)

DE Holo-(Acyl-carrier-protein) synthase (EC 2.7.8.7) (holo-ACP synthase)
 4'-phosphopantetheinyl transferase acps).

DE Name-acps; OrderedLocusNames=BCE0224;

GN Bacillus cereus (strain ZK);
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=288661;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H.;
 RA "Complete genome sequence of *Bacillus cereus* ZK.";

RT

Query Match Similarity 50.9%; Score 303; DB 1; Length 119;
 Best Local Similarity 54.7%; Pred. No. 2.7e-20; Mismatches 32; Indels 2; Gaps 1;

Matches 64; Conservative 19; MisMatches 32; Del 1; Insert 1;

QY 3 GIGLDITELKLTASMGROKPFRAERILTRSEEDOYELSERKRNFLAGRAKEAFSKA 62

RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein [By similarity].

CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine

CC -!- SUBCELLULAR LOCATION: Holo-[acyl-carrier protein] = cytoplasmic [By similarity].

CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; CP000001; AAU20010_1; - ; Genomic_DNA.

DR HAMAP; MF_00101; -; 1.

DR InterPro; IPR008278; 4-PPT_transf.

DR InterPro; IPR002582; ACPS.

DR InterPro; IPR004568; Pantethin_trans.

PFam; PF01648; ACPS; 1.

PRODom; PRO04282; ACPS; 1.

DR TIGRFAMS; TIGR00516; acps; 1.

DR TIGRFAMS; TIGR00556; pantethin_trn; 1.

KW Complete Proteome; Fatty acid biosynthesis; Lipid synthesis;

FT Magnesium; Metal-binding; Transferase.

FT METAL 8 8 Magnesium (By similarity).

FT METAL 58 58 Magnesium (By similarity).

SEQUENCE 119 AA; 13169 MW; 8730A0218813E14 CRC64;

Query Match 50.4%; Score 300; DB 1; length 119;

Best Local Similarity 53.8%; Pred. No. 5.1e-20; Matches 63; Conservative 20; Mismatches 32; Indels 2; Gaps 1;

Db 3 GIGIDITELKRIASMAGRKFAERTILTRSIDQYELSEKRKNETLAGRFAAKEFSKA 62

4 GIGIDIBELNRIKEMERILTENERNVAKGLKGSRLTEVAGRFRAKEYSKA 63

Qy 63 FGTGIGRQLSFQDIEBIRKDONGKPYIICIKLSQLQAHVHSITHKEYAAQVLERLS 119

Db 64 VGTGIGKVEFSDIEEVNDRKPILNTS--TEHTVILSHSKPEAVQVTLLESS 118

RESULT 10

ACPS_BACHD ID ACPS_BACHD STANDARD; PRT; 119 AA.

AC 09KFGI; DT 28-FEB-2003 (Rel. 41, Created)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Hololacyl-carrier-protein synthase (EC 2.7.8.7) (Holo-ACP synthase)

DE (4'-phosphopantetheineyl transferase acps).

GN Name=acps; OrderedLocusNames=BL0518;

OS Bacillus halodurans; Bacteria; Bacillaceae; Bacillus.

OC NCBI_TAXID=8665;

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=C-125 / JCM 9153; MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/gkf552; Takami H., Nakano K., Takai Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogawa N., Kuwara S., Horikoshi K., "Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*.", Nucleic Acids Res. 28:4317-4331(2000).

RL Nucleic Acids Res. 28:4317-4331(2000).

CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein [By similarity].

CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine

CC 3',5'-bisphosphate + holo-[acyl-carrier protein].

CC -!- COFACTOR: Magnesium (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic [By similarity].

CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps family.

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CC EMBL; BAB00004; BAB04237_1; - ; Genomic_DNA.

DR HSSP; Q81775; 1FTH.

DR PIR; P83714; P83714.

DR InterPro; IPR008278; 4-PPT_transf.

DR InterPro; IPR002582; ACPS.

DR InterPro; IPR004568; Pantethin_trans.

PFam; PF01648; ACPS; 1.

PRODom; PRO04282; ACPS; 1.

DR TIGRFAMS; TIGR00516; acps; 1.

DR TIGRFAMS; TIGR00556; pantethin_trn; 1.

KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;

FT MAGNESIUM; Metal-binding; Transferase.

FT METAL 8 8 Magnesium (By similarity).

SEQUENCE 119 AA; 1321 MW; 2279E52549041C9 CRC94;

Query Match 49.9%; Score 297; DB 1; Length 119;

Best Local Similarity 50.0%; Pred. No. 9.6e-20; Matches 59; Conservative 25; Mismatches 32; Indels 2; Gaps 2;

Db 3 GIGIDITELKRIASMAGRKFAERTILTRSIDQYELSEKRKNETLAGRFAAKEFSKA 62

4 GTGIDIVELERIOSKVEKHPRFKVLLTNEQEVPARLRRRLLEYTAGRFAAKEFVKA 63

Qy 63 FGTGIGRQLSFQDIEBIRKDONGKPYIICIKLSQLQAHVHSITHKEYAAQVLERLS 120

Db 64 VGTGIGKVEFSDIEEVNDRKPILNTS--TEHTVILSHSKPEAVQVTLLESS 119

RESULT 11

ACPS_LISMF ID ACPS_LISMF STANDARD; PRT; 118 AA.

AC Q72170; DT 10-MAY-2005 (Rel. 47, Created)

DT 10-MAY-2005 (Rel. 47, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Hololactyl-carrier-protein synthase (EC 2.7.8.7) (Holo-ACP synthase)

DE (4'-phosphopantetheineyl transferase acps).

GN Name=acps; OrderedLocusNames=LMO2365_0904; OS Listeria monocytogenes (Berotype 4b / Strain F2365). Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

OX NCBI_TAXID=205669;

RN [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RP Pubmed=15115801; DOI=10.1093/nar/gkh552; Nelson K.B., Routs D.E., Mongodin E.F., Ravel J., DeBoy R.T., RA Kolonay J.-P., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T., RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beaman M.J., RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R., RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N., RA Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Ulrich G.A., RA Bayles D.O., Luchansky J.B., Fraser C.M., "Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen *Listeria monocytogenes* reveal new insights into the core genome components of this species.", Nucleic Acids Res. 32:2386-2395 (2004).

CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein [By similarity].

CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine

CC 3',5'-bisphosphate + holo-[acyl-carrier protein].

CC -!- COFACTOR: Magnesium (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic [By similarity].

CC family.

-I- SIMILARITY: Belongs to the P-Pant transferrase superfamily. Acps

CC family.

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CC EMBL; AE017325; AAT03684.1; - ; Genomic_DNA.

DR

CC 3',5'-bisphosphate + holo-[acyl]-carrier protein].
 CC -!- COFACTOR: Magnesium (By similarity).
 CC -- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC EMBL; AL556166; CAC6116.1; -; Genomic_DNA.
 DR PIR; AD1543; AD1543.
 DR HSSP; P9618; 1F7L.
 DR LISTLIST; LIN00884; -.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4-PPT_transf.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantethn_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR PRODOM; PD004282; ACPS; 1.
 DR TIGRFAMS; TIGR00516; acps; 1.
 DR TIGRFAMS; TIGR00556; pantethn_trn; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Magnesium; Metal-binding; Transferase.
 PT METAL 8 8 Magnesium (By similarity).
 PT METAL 58 58 Magnesium (By similarity).
 SO SEQUENCE 118 AA; 13281 MW; BFC89CF84BCBB985 CRC64;

Query Match Best Local Similarity 51.3%; Pred. No. 1.9e-18; Mismatches 39; Indels 0; Gaps 0;
 Matches 59; Conservativeness 17; Mismatches 39; Indels 0; Gaps 0;

Qy 3 GIGLDITTELKRITASMACRQRKRAERILTRSEDOYELSERKEKNFLAGRAEAKAFSKA 62
 Db 4 GIGLDWMDLDRKIQAVENKNPRIERLITEKEIKQVKEYGSKRKTFLAGRAEKAYKA 63

RESULT 14
 ACPS_STAEQ STANDARD; PRT; 117 AA.

AC ID 08CNK6; 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-[acyl]-carrier-protein synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN Name=acps; OrderedLocusName=SRR1684;
 OS Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
 RN [1] NCBI_TaxID=176279;

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
 RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
 RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
 RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
 RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
 RA Dimitrov G., Jiang L., Qin H., Waldman J., Tran K., Kang K.H.,
 RA Dimitrov I.R., Nelson K.E., Fraser C.M.;
 RT "Insights on evolution of virulence and resistance from the complete genome analysis of an early methicillin-resistant Staphylococcus aureus strain and a biofilm-producing methicillin-resistant Staphylococcus epidermidis strain.";
 RT J. Bacteriol. 187:2426-2438 (2005).
 RL Mol. Microbiol. 49:1577-1593 (2003).
 CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein (By similarity).
 CC A to a Ser of acyl-carrier protein (By similarity).
 CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl]-carrier protein] = adenosine 3',5'-bisphosphate + holo-[acyl]-carrier protein.
 CC -!- COFACTOR: Magnesium (By similarity).
 CC 3',5'-bisphosphate + holo-[acyl]-carrier protein.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps family.

CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC EMBL; AEO16749; AA005274.1; -; Genomic_DNA.
 DR HSSP; P9618; 1F7L.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4-PPT_transf.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantethn_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR PRODOM; PD004282; ACPS; 1.
 DR TIGRFAMS; TIGR00516; acps; 1.
 DR TIGRFAMS; TIGR00556; pantethn_trn; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Magnesium; Metal-binding; Transferase.
 PT METAL 8 8 Magnesium (By similarity).
 PT METAL 58 58 Magnesium (By similarity).
 SO SEQUENCE 117 AA; 13285 MW; 5124561C1CDBDCG_CRC64;

Query Match Best Local Similarity 51.3%; Pred. No. 4e-18; Mismatches 30; Indels 9; Gaps 4;
 Matches 61; Conservativeness 19; Mismatches 30; Indels 9; Gaps 4;

Qy 2 YGIGLDITTELKRITASMACRQRKRAERILTRSEDOYELSERKEKNFLAGRAEAKFA 58
 Db 3 YGIGLDWMDLDRKIQAVENKNPRIERLITEKEIKQVKEYGSKRKTFLAGRAEKAYKA 59
 Qy 59 FSKAIGTGTGIGRSQDIELRKDQNGPKYIICLKLSQAVHSVTHTKEYAAQWVIER 117
 Db 60 FSKAIGTGTGIGKSVSQDINCYNDALGKP---CIDIYPGYTHVSHTHTENYAMQVILER 115

RESULT 15
 ACPS_STAEQ STANDARD; PRT; 117 AA.

AC ID 05HNE4; 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-[acyl]-carrier-protein synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN Name=acps; OrderedLocusName=SRR1684;
 OS Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
 RN [1] NCBI_TaxID=176279;

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
 RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
 RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
 RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
 RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
 RA Dimitrov G., Jiang L., Qin H., Waldman J., Tran K., Kang K.H.,
 RA Dimitrov I.R., Nelson K.E., Fraser C.M.;
 RT "Insights on evolution of virulence and resistance from the complete genome analysis of an early methicillin-resistant Staphylococcus aureus strain and a biofilm-producing methicillin-resistant Staphylococcus epidermidis strain.";
 RT J. Bacteriol. 187:2426-2438 (2005).
 RL Mol. Microbiol. 49:1577-1593 (2003).
 CC -!- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme A to a Ser of acyl-carrier protein (By similarity).
 CC A to a Ser of acyl-carrier protein (By similarity).
 CC -!- CATALYTIC ACTIVITY: CoA + apo-[acyl]-carrier protein] = adenosine 3',5'-bisphosphate + holo-[acyl]-carrier protein.
 CC -!- COFACTOR: Magnesium (By similarity).
 CC 3',5'-bisphosphate + holo-[acyl]-carrier protein.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps family.

CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
 CC CC the European Bioinformatics Institute. There are no restrictions on its
 CC CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; CP000029; AAW55047.1; -; Genomic_DNA.
 DR TIGRFAMS; SRP1684; -.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4_PPT_transf.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantethin_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMS; TIGR00516; acPS; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Magnesium; Metal-binding; Transferease.
 FT METAL 8 8 Magnesium (By similarity).
 METAL 58 58 Magnesium (By similarity).
 SEQUENCE 117 AA; 13535 MW; 515246BC1C4DEDCA9 CRC64;

Query Match 47 0%; Score 279.5; DB 1; Length 117;
 Best Local Similarity 51.3%; Pred. No. 4e-18; Gaps 4
 Matches 61; Conservative 19; Mismatches 30; Indels 9; QY 2 YGIGIDITEKLRIKASMGQRKFRAERILIT--RSELDQYYELSEKRKNFAGRPAAKER 58
 3 YGIGIDLIEERIPIKIQ-NQTKFIERLIEERDKNQY-TheorieFLAGHFTVKEA 59

QY 59 FSKAGTGTGKSVFQDINCYNDALGKB--CIDYPGFYTHSITHTENYAMSQVILEK 117
 60 FSKAGTGTGKSVFQDINCYNDALGKB--CIDYPGFYTHSITHTENYAMSQVILEK 115

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OM protein - protein search, using sw model	GenCore version 5.1.6	
Run on:	Copyright (c) 1993 - 2005 Compugen Ltd.	
	December 21, 2005, 13:40:44 ; Search time 15.5224 Seconds	
	(without alignments)	
	743.830 Million cell updates/sec	
Title:	US-10-717-138-2	
Perfect score:	595	
Sequence:	1 AYGIGLGLDTTELKRKIASMAGR..... SITHIKSYAAQWIERLSS 120	
Scoring table:	BLOSUM62	
	Gapop 10.0 , Gapext 0.5	
Searched:	283416 seqs, 96216763 residues	
Total number of hits satisfying chosen parameters:	283416	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	PIR 80:** 1: pir1:** 2: pir2:** 3: pir3:** 4: pir4:**	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
Result No.	Score	Query Match Length DB ID Description
1	591	99.3 121 1 H69772 holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) - <i>Bacillus subtilis</i>
2	49.9	119 2 F83714 holo-[acyl-carrier
3	48.2	118 2 AE1185 holo-acyl-carrier
4	28.3	47.6 118 2 AD1543 holo-acyl-carrier
5	27.5	46.2 119 2 E89943 holo-ACP synthase
6	26.1	43.9 119 2 C86730 acyl carrier pro
7	24.3	40.8 120 2 H95197 holo-acyl-carrier
8	24.3	40.8 120 2 D98064 holo-acyl-carrier
9	23.7.5	39.9 126 2 F82072 holo-acyl-carrier
10	22.1.5	37.2 124 2 B93960 holo-acyl-carrier
11	201.5	33.9 169 2 F7245 holo-[acyl-carrier
12	201	33.8 126 2 F71562 holo-[acyl-carrier
13	199.5	33.7 126 2 AF0556 holo-[acyl-carrier
14	195.5	32.9 126 2 E91057 hypothetical prote
15	192.5	32.4 126 2 B85502 hypothetical prote
16	192.5	32.4 126 2 AG0838 holo-[acyl-carrier
17	189.5	31.8 126 1 F42294 holo-[acyl-carrier
18	189	31.8 131 2 A97910 hypothetical prote
19	188.5	31.7 126 2 F84952 holo-[acyl-carrier
20	180.5	30.3 119 2 C71556 holo-[acyl-carrier
21	178.5	30.0 125 2 D81833 holo-[acyl-carrier
22	177.5	29.8 122 2 A86530 acyl-carrier prote
23	177.5	29.8 122 2 B7203 holo-[acyl-carrier
24	173.5	29.2 125 2 D81710 holo-[acyl-carrier
25	173	29.1 125 2 F71276 holo-[acyl-carrier
26	168.5	28.3 125 2 F81197 holo-[acyl-carrier
27	166.5	28.0 119 1 H64620 holo-[acyl-carrier
28	162.5	27.3 191 2 AC3413 holo-[acyl-carrier
29	161.5	27.1 119 2 G71894 holo-[acyl-carrier
RESULT 1		
H69772		
C;Species: <i>Bacillus subtilis</i>		
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004		
C;Accession: H69772		
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F.; Ichel, J.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, Y.; Ogawa, K.; Ochiai, A.; Outogawa, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadai, Y.; Sato, T.; Scanlon, A.; Schleicher, S.; Schroeter, R.; Scuffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.		
A;Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i>		
A;Reference number: A69580; PMID:98044033; PMID:9384377		
A;Accession: H69772		
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown		
A;Molecule type: DNA		
A;Residues: 1-121 <KIN>		
A;Cross References: UNIPROT:P96118; UNIPARC:UPI000005FF70; GB:Z99106; GB:AL009126; NID:		
A;Experimental source: strain 168		
C;Genetics:		
A;Gene: ydb		
C;Superfamily: holo-ACP synthase		
C;Keywords: coenzyme A; transferase		
Query Match	99.3%; Score 591; DB 1; Length 121;	
Best Local Similarity	100.0%; pred. No. 4.8e-52;	
Matches	119; Conservative 0; Mismatches 0; Index 0; Gaps 0;	
OY	2 YGIGLGLDTTELKRKIASMAGRQKFAERTLTTSRSLDQQYELSEKRNKNFLGAFRAKEAPSK 61	
QY	3 YGGGLDTTELKRKIASMAGRQKFAERTLTTSRSLDQQYELSEKRNKNFLGAFRAKEAPSK 62	
Db	62 ARCTGTGRQLSFDIERTKDONGKPYIICTKLSQAQHVSITHKEYAAQWIERLSS 120	
Db	63 ARGTGIGRQLSFDIERTKDONGKPYIICTKLSQAQHVSITHKEYAAQWIERLSS 121	
RESULT 2		
F83714	holo-[acyl carrier protein] synthase BH0518 [imported] - <i>Bacillus halodurans</i> (strain C-1)	
C;Species: <i>Bacillus halodurans</i>	C;Accession: F83714	
C;Accession: F83714	C;Accession: F83714	

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai, N.; Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: F83714
 A;Status: preliminary
 C;Gene: BH0518
 A;Molecule type: DNA
 C;Superfamily: holo-ACP synthase

Query Match 49.9%; Score 297; DB 2; Length 119;
 Best Local Similarity 50.0%; Pred NO. 1.2e-22;
 Matches 59; Conservative 25; Mismatches 32; Indels 2; Gaps 2;

QY 3 GIGLIDITEKLRIASAGRQRFAFRLITSELQYELSEKRKRFQFLAGRFAAKERAFSKA 62
 Db 4 GTGIDIVELERIOTSNVEKHPFRVKILTENEQEVARLSRNRRLYTAQRFKAFAVKA 63
 QY 63 FGIGIGRQLSFDQFDEIRKQDONGKPYIICKLKSQAMVHSITHTKEYAAQWVIRELS 120
 Db 64 VGRGISAEXQWHDLIEVLUSBRGKP-VLSVNL-DATIHWGSHSQSYAIQVILERLSS 119

RESULT 3

AB1185 holo-acyl-carrier protein synthase homolog lmo0885 [imported] - *Listeria monocytogenes* C;Species: *Listeria monocytogenes*
 C;Accession: AB1185
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kuraplat, G.; Madueno, E.; Maitouram, A.; Ma, C.; Schlueter, T.; Simoes, N.; Tiercer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of *Listeria* species
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AB1185
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-118 <GTO>
 A;Cross-references: UNIPROT:Q8Y8L2; UNIPARC:UPI0000054DAF; GB:NC_003210; PIDN:CAC98963.1
 A;Experimental source: strain EGD-e
 A;Genetics:
 C;Superfamily: holo-ACP synthase

Query Match 48.2%; Score 287; DB 2; Length 118;
 Best Local Similarity 50.9%; Pred. NO. 1.2e-21;
 Matches 58; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 3 GIGDITEKLRIASAGRQRFAFRLITSELQYELSEKRKRFQFLAGRFAAKERAFSKA 62
 Db 4 GIGDMDLDERVKQVEKNPFRFIERVTEKEIKQDFEKEYENRKDFLAGFAEKAYKA 63
 QY 63 FGTGIGRQLSFDQFDEIRKQDONGKPYIICKLKSQAMVHSITHTKEYAAQWIE 116
 Db 64 NGTGPKHLSFTDVILQVEDGRPHAVTLPVKSGENVFVSITHARSAAGVIE 117

RESULT 4

AD1543 holo-acyl-carrier protein synthase homolog lmo0884 [imported] - *Listeria innocua* (strain C;Species: *Listeria innocua* C;Accession: AD1543 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurakata, G.; Madiueno, E.; Maitourneau, A.; Matz, C.; Schlueter, T.; Simoes, N.; Terrier, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Title: Comparative genomics of *Listeria* species
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AD1543
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-118 <KUR>
 A;Cross-references: UNIPROT:Q92DPO; UNIPARC:UPI000125338; GB:AL592022; PIDN:CAC96116.1;
 A;Experimental source: strain Clp1262
 C;Genetics:
 A;Gene: lin0884
 C;Superfamily: holo-ACP synthase
 Query Match 47.6%; Score 283; DB 2; Length 118;
 Best Local Similarity 51.3%; Pred. No. 3.1e-21;
 Matches 59; Conservative 17; Mismatches 39; Indexes 0; Gaps 0;
 Qy 3 GIGIDITTEKRIASMAGRQFRARFLTSRSELQYELSEKRRKPFLAGPFAKAFSKA 62
 4 GIGIDMDILDRVKQAVENPKPRFIERLITEKETKQYKEVGSRKKFAGFAKEAYAKA 63
 Qy 63 FGCGIGRQLSFDQPIERIKDONGKYYTICKLSQAVHVSHTKEYAAQWIER 117
 64 NGTGRGKGKILSPDVFILQVEDGRPRHVTMPKQGETVFSITHTARSAQAQVIEQ 118
 RESULT 5
 E89999 holo-ACP synthase [imported] - *Staphylococcus aureus* (strain N315)
 C;Species: *Staphylococcus aureus*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C;Accession: E89999
 R.Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A;Reference number: A89758; MUID:2131952; PMID:11418146
 A;Accession: E89999
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-119 <KUR>
 A;Cross-references: UNIPROT:Q99ST4; UNIPARC:UPI000125346; GB:BA000018; PID:g13701866;
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: dpj
 C;Superfamily: holo-ACP synthase
 Query Match 46.2%; Score 275; DB 2; Length 119;
 Best Local Similarity 48.7%; Pred. No. 2e-20;
 Matches 57; Conservative 24; Mismatches 32; Indexes 4; Gaps 2;
 Qy 2 YGIGIDITEKLRIASMAGRQFRARFLTSRSELQYELSEKRRKPFLAGPFAKAEFS 60
 3 HGIGDILDEIDRKLQYKQPKLVERILTGNEQHKFNNTHEORKIEFLAGPFAKEAFS 62
 Qy 61 KAFGTGIGRQLSFDQPIERIKDONGKYYTICKLSQAVHVSHTKEYAAQWIER 117
 63 KALGGGLGKGKILSPDVFILQVEDGRPRHVTMPKQGETVFSITHTARSAQAQVIEQ 118
 RESULT 6
 C86730 acyl carrier protein synthase [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL14
 C;Species: *Lactococcus lactis* subsp. *lactis*
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C;Accession: C86730
 R.Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, S.; Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* subsp. *lactis*
 A;Reference number: A86252; MUID:21230186; PMID:11337471

A;Accession: CG6730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-120 <KUR>
A;Cross-references: UNIPROT:Q9CH95; UNIPARC:UPI0000125336; GB:AE005176; PID:gi12723769; E

C;Genetics:
A;Experimental source: strain TII403
C;Genetics:
A;Gene: acPS
C;Superfamily: holo-ACP synthase

Query Match 43.9%; Score 261; DB 2; Length 119;
Best Local Similarity 49.2%; Pred. No. 5e-19; Mismatches 37; Indels 4; Gaps 3;
Matches 58; Conservative 19; Mismatches 31; Indels 10; Gaps 3;

Qy 2 YGIGLDTIELKKITASMAKGRO-KRFAERILTRSELDQYEL-SEKRKNFELLAGRAFAKEAFS 60
Db 3 FGTGVQVNEVELSIQKALTRSERPVEQLTAVALEKINSPOSTARKBQFLAGRWAKAEFS 62

Qy 61 KAFGTGIGROLQSFDQFDEIRKQDONGKPVIICTKLS-QAAVHVSITHKEYAAQVIER 117
Db 63 KAYGTGFGKALGMHDLBKNDLGKPF--TKHPFDGQVHLSISHNLEAVAFVULEK 118

RESULT 7

H95197
holo-(acyl-carrier protein) synthase [imported] - Streptococcus pneumoniae (strain TIGR4

C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: H95197
R;Tetelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidorn, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, T.; Hickey, E.K.; Holt, T.E. Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95197
A;Status: preliminary
A;Cross-references: UNIPROT:Q9FTTS; UNIPARC:UPI000005195A; GB:AE005672; PIDN:AAK75777.1;
A;Gene: SPt699
A;Experimental source: strain TIGR4
C;Genetics:
C;Superfamily: holo-ACP synthase

Query Match 40.8%; Score 243; DB 2; Length 120;
Best Local Similarity 44.1%; Pred. No. 3.2e-17; Mismatches 31; Indels 10; Gaps 3;
Matches 52; Conservative 25; Mismatches 31; Indels 10; Gaps 3;

Qy 3 GIGLDTIELKKITASMAKGRO-KRFAERILTRSELDQYEL-SEKRKNFELLAGRAFAKEAFS 62
Db 4 GHGIDIEELIASIESAVTRHEGFKVLTQAEMRFTSKGRROTEYLAGRWSAKEASKA 63

Qy 63 FGNGIGROLQSFDQFDEIRKQDONGKPVIICTKLS-QAAVHVSITHKEYAAQVIE 116
Db 64 MGTGISK-LGFQDLEVLNNERGAPY----FSQAPFSKWIISIHTDQFVTASVILE 115

RESULT 8

D98064
holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) [imported] - Streptococcus pneumoniae

C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: D98064
R;Hoskins, J.A.; Albion Jr., W.; Arnold, J.; Blazczak, L.; Burgett, S.; Dehoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsumura, P.; McAhren, S.; M; Y.; Sun, P.M.; Winkler, M.B. J. Bacteriol. 183, 5705-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D98064

RESULT 9

F82072
holo-(acyl-carrier-protein) synthase vc2457 [imported] - vibrio cholerae (strain N16961)

C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82072
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Emamiya, M.D.; Vanathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: F82072
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-126 <HIN>
A;Cross-references: UNIPROT:Q9KPB6; UNIPARC:UPI000012534D; GB:AE004316; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2457
C;Map position: 1
C;Superfamily: holo-ACP synthase

Query Match 39.9%; Score 237.5; DB 2; Length 126;
Best Local Similarity 42.7%; Pred. No. 1.2e-16; Mismatches 36; Indels 11; Gaps 3;
Matches 53; Conservative 24; Mismatches 36; Indels 11; Gaps 3;

Qy 3 GIGLDTIELKKITASMAKGRO-KRFAERILTRSELDQYEL-SEKRKNFELLAGRAFAKEAFS 61
Db 4 GLGIDIEELIASIESAVTRHEGFKVLTQAEMRFTSKGRROTEYLAGRWSAKEASK 61

Qy 62 AFGTGIGROLQSFDQFDEIRKQDONGKPVIICTKLS-QAAVHVSITHKEYAAQV 113
Db 62 ALGTGIAQGVTFHDFTSHDKUGKPLILSGQAEELASOLOVENIHLISIDERHYMATV 121

Qy 114 VIER 117
Db 112 ILER 125

RESULT 10

B86960
holo-acyl-carrier protein synthase [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B86960
R;Nolling, J.; Breton, G.; Omelichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Kotin, E.V.; Smith, D.R. J. Bacteriol. 183, 4323-4338, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B96960
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9ZC55; UNIPARC:UPI0000125344; GB:AJ235272; GB:AJ235269; NID
A;Experimental source: strain Madrid E
A;Genetics:
C;Superfamily: holo-ACP synthase
C;Keywords: coenzyme A; transferase

Query Match 33.8%; Score 201; DB 2; Length 126;
Best Local Similarity 40.0%; Pred. No. 5.4e-13; Gaps 2;
Matches 48; Conservative 21; Mismatches 45; Indels 6; Gaps 2;

Qy 3 GIGUDITELKRIASMGAGRQKFAERILTRSLDQYELSERKNEFLAGRFAKEASFKA 61
Db 4 GVGVDLIEINRVKAIDRNVYKPIEKLFPSRRLI--AYTAKETKQAQYTAGRSKEAVSKA 61

Qy 63 FGTGIGROLSQDIERKQDONGKPYIICTKSQA-----AVHVSITHKEYAAQVV 114
Db 62 LGTGF-RGFSFVNIEHKDDGKPTIVWLNGARATAEGYGYQVQLSISHREKAJAV 120

Qy 115 IIE 116

Db 121 IIE 122

RESULT 11

B72345 holo-[acyl carrier protein] synthase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72345
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Grinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 322-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <ARN>
A;Cross-references: UNIPROT:Q9WZF6; UNIPARC:UPI0000125349; GB:AE001741; GB:AE000512; NID
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0692

Query Match 33.9%; Score 201.5; DB 2; Length 169;
Best Local Similarity 42.4%; Pred. No. 6.7e-13; Gaps 7;
Matches 50; Conservative 23; Mismatches 30; Indels 15; Gaps 7;

Qy 3 GIGUDITELKRIASMGAGRQKFAERILTRSLDQYELSERKNEFLAGRFAKEASFKA 62
Db 4 GVGIDVLEEVERV-----PERFAERILGESKRLF--LTRKRRBETAGFALKERAFFKA 55

Qy 63 FGTGIGROLSQDIERKQDONGKPYIICTKSQA---AVHVSITHKEYAAQVTER 117
Db 56 LGTGLNKH-SFTDVEF-LESNSKPK-VLCVHKGFFNYAHVSLSHDR-FAVALVLEK 109

RESULT 12

F71652 holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) RP577 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Accession: F71652
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: F71662
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U; Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:9039499; PMID:9823893
A;Accession: F71662
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-126 <AND>
A;Cross-references: UNIPROT:Q9ZC55; UNIPARC:UPI0000125344; GB:AJ235272; GB:AJ235269; NID
A;Experimental source: strain Madrid E
A;Genetics:
C;Superfamily: acPS
C;Keywords: holo-ACP synthase

Query Match 33.8%; Score 201; DB 2; Length 126;
Best Local Similarity 40.0%; Pred. No. 5.4e-13; Gaps 2;
Matches 48; Conservative 21; Mismatches 45; Indels 6; Gaps 2;

Qy 3 GIGUDITELKRIASMGAGRQKFAERILTRSLDQYELSERKNEFLAGRFAKEASFKA 61
Db 4 GVGDIVQTPRIEKLNIVOLEFAKKILAKELQFTLJNKTHATFLAKRFSKEAVSK 63

Qy 62 AFGTGIGROLSQDIERKQDONGKPYI-----ICTKLQSQAVHVSITHKEYAAQVTE 116
Db 64 AFGVGIGRGINFKDITLNDNLGKPTVEISSHYTNKLAPPNHLSSLSDYDPICTAFAIE 123

RESULT 13

AF0356 holo-[acyl-carrier protein] synthase (EC 2.7.8.7) [imported] - Yersinia pestis (strain CC)
C;Species: Yersinia pestis
C;Accession: AF0356
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B., deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:1156360

A;Accession: AF0356
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-126 <KUR>
A;Cross-references: UNIPROT:Q8ZCP5; UNIPARC:UPI000012534E; GB:AL590842; PIDN:CAC92177.1;
C;Genetics:
A;Gene: acPS
C;Superfamily: holo-ACP synthase
C;Keywords: coenzyme A; transferase

Query Match 33.7%; Score 200.5; DB 2; Length 126;
Best Local Similarity 39.0%; Pred. No. 6e-13; Gaps 43; Indels 11; Gaps 3;
Matches 48; Conservative 21; Mismatches 43; Indels 11; Gaps 3;

Qy 3 GIGUDITELKRIASMGAGRQKFAERILTRSLDQYELSERKNEFLAGRFAKEASFKA 61
Db 5 GUGTDIVLSEIRQAVERTGERLARRILSPSEWHYQO--HQOPVRFLKRFVKEAMK 62

Qy 62 AFGTGIGROLSQDIERKQDONGKPYI-----ICTKLQSQAVHVSITHKEYAAQV 113
Db 63 AFGTGIGRNLAFNFQEVVNDALGKPTLRLHSRAELAVELGVKSLHVTLADERRYACAV 122

Qy 114 VIE 116
Db 123 IIE 125

RESULT 14

E91057 hypothetical protein ECS3429 [imported] - Escherichia coli (strain O157:H7, substrain RI)
C;Species: Escherichia coli
C;Accession: E91057
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E91057
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasavara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.; DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11255796
A;Accession: E91057

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-126 <HAY>
A;Cross-references: UNIPROT:Q8XA39; UNIPARC:UPI00001654C5; GB:BA000007; PIDN:BAB36852.1;
A;Experimental source: strain O157:H7, substrain RIMD 050952
C;Genetics:
A;Gene: Ecs3429
C;Superfamily: holo-ACP synthase

Query Match 32.9%; Score 195.5; DB 2; Length 126;
Best Local Similarity 38.2%; Pred. No. 1.9e-12; Indels 11; Gaps 3;
Matches 47; Conservative 23; Mismatches 42; Indels 11; Gaps 3;

Qy 3 GIGLDITELKIRASMGAGRQ-KRFAERILTRBLDQYELSEKKRNFLAGRAKEAFSK 61
Db 5 GIIGTDIVELKIRAEVIAVRSGRLLRRLVTSNEWETW--KTHHQPVFLAKRFAVKAAK 62

Qy 62 AFGTGIGRQLRQDIEIRKQDNGKPYI-----ICTKLSQAVAVSITTKEMAAQ 113
Db 63 AFGTGIRGNGLAFNQFEVFNDELGKPRLRWSEALKLAEGKSYANMVTLADERHYACTV 122

Qy 114 VIE 116
Db 123 IIE 125

RESULT 15

B85902 hypothetical protein acps [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: B85902
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotnbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-126 <STOP>
A;Cross-references: UNIPARC:UPI00001658C8; GB:AB005174; NID:912516980; PIDN:AAG57678.1;
A;Experimental source: strain O157:H7, substrain EDL93
C;Genetics:
A;Gene: acps
C;Superfamily: holo-ACP synthase

Query Match 32.4%; Score 192.5; DB 2; Length 126;
Best Local Similarity 38.2%; Pred. No. 3.8e-12; Indels 11; Gaps 3;
Matches 47; Conservative 22; Mismatches 43; Indels 11; Gaps 3;

Qy 3 GIGLDITELKIRASMGAGRQ-KRFAERILTRBLDQYELSEKKRNFLAGRAKEAFSK 61
Db 5 GIIGTDIVELKIRAEVIAVRSGRLLRRLVTSNEWETW--KTHHQPVFLAKRFAVKAAK 62

Qy 62 AFGTGIGRQLRQDIEIRKQDNGKPYI-----ICTKLSQAVAVSITTKEMAAQ 113
Db 63 AFGTGIRGNGLAFNQFEVFNDELGKPRLRWSEALKLAEGKSYANMVTLADERHYACTV 122

Qy 114 VIE 116
Db 123 IIE 125

Search completed: December 21, 2005, 13:49:39
Job time : 16.5224 secs

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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:40:03 ; Search time 158.806 Seconds
 (without alignments)
 332.012 Million cell updates/sec

Title: US-10-717-138-2

Perfect score: 595
 Sequence: 1 AYKIGLGLDTIELKKIASMAGR.....SITHTKYAAQVWIERLSS 120

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:

2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqP1930s:*

2: geneseqP1930s:*

3: geneseqP2000s:*

4: geneseqP2001s:*

5: geneseqP2002s:*

6: geneseqP2003as:*

7: geneseqP2003bs:*

8: geneseqP2004s:*

9: geneseqP2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

RESULT	1
ID	AAU10694 standard; protein; 120 AA.
AC	AAU10694;
XX	
XX	25-FEB-2002 (first entry)
DE	B. subtilis ACPS used to grow ACP/ACPS complex crystals.
XX	Crystal structure; acyl carrier protein synthase; acyl carrier protein; rational drug design method; antibiotic; 4'-phosphopantetheinyl; P-pant; ACP/ACPS complex; protein co-ordinate data.
XX	OS Bacillus subtilis.
XX	PN WO200185743-A2.
XX	PD 15-NOV-2001.
PF	26-JAN-2001; 2001WO-US002949.
PR	08-MAY-2000; 2000US-0202466P.
XX	(AMHPC) AMERICAN HOME PROD CORP.
PA	(MILL-) MILLENNIUM PHARM INC.
XX	PI Parris KD, Somers WS, Tam AS, Lin LL, Stahl ML, Powers R, Xu G;
XX	DR WPI; 2002-055580/07.
XX	PT Crystallized complex useful in rational drug design methods, comprises acyl carrier protein synthase and acyl carrier protein.
XX	PS Example 1; Fig 1; 147pp; English.
CC	The present invention relates to a crystallised structure comprising acyl carrier protein synthase (ACPS) complexed with acyl carrier protein (ACP). The invention also describes the solution structure of <i>Bacillus subtilis</i> ACP. Both these structures are useful in rational drug design methods for identifying agents that may interact with active sites of ACPS and ACP, and for testing these agents to identify agents that may represent novel antibiotics. They are also useful for design and selection of potent and selective agents which interact with ACPS and ACP, and for the design of antibiotics and other agents that interfere with 4'-phosphopantetheinyl (P-pant) attachment, thus preventing activation of corresponding carrier proteins. The present sequence

25 262 44.0 126 6 ABU24470

26 261 43.9 119 5 ABB5157

27 260 43.7 129 7 ADC97363

28 250 42.0 117 6 ADB06134

29 250 42.0 117 8 ADJ27057

30 241 41.0 113 6 ADB06132

31 243 40.8 120 3 AAY58607

32 243 40.8 120 6 ABU2175

33 243 40.8 120 6 ABU4200

34 243 40.8 120 8 ADK46642

35 243 40.8 122 2 AAW8012

36 243 40.8 122 4 AAU77879

37 243 40.8 122 4 AAU38056

38 243 40.8 122 7 ADB34480

39 243 40.8 123 6 ABR83307

40 243 40.8 123 6 ABR83308

41 243 40.8 156 3 AAY88388

42 243 40.8 157 8 ADR95564

43 243 40.8 126 6 ABR49557

44 237.5 39.9 119 3 AAY91289

45 228.5 38.4 119 3 AAY91289

ALIGNMENTS

Abc24470 Protein e

Abb5157 Lactococc

Adc97363 E. faeciu

Adb06134 Alloiococ

Adj27057 Alloiococ

Aaw8012 Alloiococ

Aay58607 Streptoco

Abu2175 S. pneumo

Abu4200 Protein e

Adk46642 Streptoco

Aaw8012 S. pneumo

Aau77879 Streptoco

Aau38056 Streptoco

Abd37480 S. pneumo

Abx33307 S. pneumo

Abx33308 S. pneumo

Aay88388 S-ydcB es

Adr95564 Novel S.

Aea59434 Streptoco

Abu9557 Protein e

Aay91289 Group B S

CC represents *B. subtilis* ACPS used to grow ACP/ACPS complex crystals
 XX Sequence 120 AA;
 SQ

Query Match 100.0%; Score 595; DB 5; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYGIGDITEKLRIASMAGRQRKFAERILITRSQDYYELSEKRNEFLAGRAKEAFS 60
 Db 1 AYGIGDITEKLRIASMAGRQRKFAERILITRSQDYYELSEKRNEFLAGRAKEAFS 60

QY 61 KAFGTGIGRQLSFQDIEIRKDONGKPYIICTKLSQAQVHSITHKEYAAQVIERLSS 120
 Db 61 KAFGTGIGRQLSFQDIEIRKDONGKPYIICTKLSQAQVHSITHKEYAAQVIERLSS 120

RESULT 2
 AAY88389
 ID AAY88389 standard; protein; 121 AA.
 XX
 AC AAY88389;
 XX
 DT 25-JUL-2000 (first entry)
 DE B-ydcB essential bacterial protein amino acid sequence.
 XX
 KW Bacterial gene; B-YdcB; Streptococcus pneumoniae; antibacterial compound; acyl carrier protein synthase; identify; bacterial infection; treatment.
 KW
 OS *Bacillus subtilis*.
 XX
 PN WO200018952-A1.

XX
 PD 06-APR-2000.
 XX
 PP 30-SEP-1999; 99WO-US022666.
 XX
 PR 30-SEP-1998; 98US-00163446.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PT Fritz C, Youngman P, Guzman L;
 DR WPI: 2000-303457/26.
 DR N-PSDB; AAI13271.

XX
 PT Identifying new antibacterial agents particularly against *Streptococcus pneumoniae*, uses S-YdcB polypeptide from *S. pneumoniae* and B-YdcB polypeptide from *Bacillus subtilis*.
 XX
 PS Claim 17; Fig 2; 58pp; English.

XX
 CC This sequence represents the essential bacterial protein B-ydcB from *Bacillus subtilis*. B-ydcB is an ortholog of the S-YdcB from *Streptococcus pneumoniae*. The gene encodes a protein which has structural characteristics of acyl carrier protein synthase and displays synthase activity in vitro. The protein is used in a method for identifying an antibacterial agent, which comprises contacting an S-YdcB or B-ydcB polypeptide with a test compound and detecting an interaction between the polypeptide and the test compound, where the interaction indicates that the compound is an antibacterial compound. Antibacterial agents identified using the method may be used to treat a bacterial infection, especially *Streptococcus pneumoniae* in mammals, especially a human or rodent. The method can be configured for high throughput screening of numerous candidate antibacterial agents, and identified agents should have a broad spectrum of antibacterial activity
 XX
 SQ Sequence 121 AA;

Query Match 99.3%; Score 591; DB 3; Length 121;
 Best Local Similarity 100.0%; Pred. No. 5.9e-63;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITEKLRIASMAGRQRKFAERILITRSQDYYELSEKRNEFLAGRAKEAFS 61
 Db 3 YGIGDITEKLRIASMAGRQRKFAERILITRSQDYYELSEKRNEFLAGRAKEAFSK 62

QY 62 AFGTGIGRQLSFQDIEIRKDONGKPYIICTKLSQAQVHSITHKEYAAQVIERLSS 120
 Db 63 AFGTGIGRQLSFQDIEIRKDONGKPYIICTKLSQAQVHSITHKEYAAQVIERLSS 121

RESULT 3
 AAMS2130
 ID AAMS2130 standard; protein; 121 AA.
 XX
 AC AAMS2130;
 XX
 DT 01-FEB-2002 (first entry)
 DE *Bacillus subtilis* ACPS.
 XX
 KW *Bacillus subtilis*; ACPS; acyl carrier protein synthase; active site; protein coordinate data; CoA binding site; X-ray crystallography; Swiss Protein P96618.
 XX
 OS *Bacillus subtilis*.
 XX
 PN WO200155340-A2.

XX
 PD 02-AUG-2001.
 XX
 PR 26-JAN-2001; 2001WO-US002732.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Parris KD, Somers WS, Tam AS, Lin LL, Stahl ML;
 XX
 DR WPI; 2001-476201/51.
 XX
 PT Novel crystallized acyl carrier protein synthase enzyme used to identify an activator or inhibitor of a molecule or complex comprising a CoA binding site, and to determine the molecular structure of a molecule or protein complex.
 XX
 PG Disclosure; Fig 8; 181pp; English.
 XX
 CC The invention relates to a crystallized acyl carrier protein synthase (ACPS) enzyme used to identify an agent that interacts with the active site, to identify an activator or inhibitor of a molecule or molecular complex comprising a CoA binding site and to determine the molecular structure. The present sequence is that of the *Bacillus subtilis* ACPS
 CC
 SQ Sequence 121 AA;

Query Match 99.3%; Score 591; DB 4; Length 121;
 Best Local Similarity 100.0%; Pred. No. 5.9e-63;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITEKLRIASMAGRQRKFAERILITRSQDYYELSEKRNEFLAGRAKEAFS 61
 Db 3 YGIGDITEKLRIASMAGRQRKFAERILITRSQDYYELSEKRNEFLAGRAKEAFSK 62

QY 62 AFGTGIGRQLSFQDIEIRKDONGKPYIICTKLSQAQVHSITHKEYAAQVIERLSS 120
 Db 63 AFGTGIGRQLSFQDIEIRKDONGKPYIICTKLSQAQVHSITHKEYAAQVIERLSS 121

RESULT 4
 ABU18305
 ID ABU18305 standard; protein; 119 AA.
 XX
 PT Query Match 99.3%; Score 591; DB 3; Length 121;
 Best Local Similarity 100.0%; Pred. No. 5.9e-63;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ABU18305;
 XX
 DT 19-JUN-2003 (First entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #3822.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Bacillus anthracis.
 XX
 PN WO20071183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PP 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-0094893.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELTRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACI22175.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 PT
 PS Claim 25; SEQ ID NO 46229; 176pp; English.

XX
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 Sequence 119 AA;

XX
 Query 3 GIGIDITTELKRITASMGKGRKAESRILITSELDQYSEKRNKEFLGAFKA 62
 Db 4 GIGIDITTELKRITASMGKGRKAESRILITSELDQYSEKRNKEFLGAFKA 63
 Query 63 FGTGIGRQLSFDQDFIRKGKPDONGKPIICTKLQAVHVSITHGEYAAQVFLRS 120
 Db 64 VGTGIGKEVSPFLDEVRNDDRGKPLITS--TEHVHLSTHSKEFAVAQVVLSSS 119

RESULT 5
 ABB47581
 ID ABB47581 standard; protein; 118 AA.
 XX
 ABB47581;
 XX
 DT 05-FEB-2002 (first entry)
 DE Listeria monocytogenes protein #285.
 XX
 Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; Vitamin B12; bacterial infection; disease.
 XX
 OS Listeria monocytogenes.
 XX
 WO200177335-A2.
 DN
 PD 18-OCT-2001.
 XX
 PR 11-APR-2001; 2001WO-FR001118.
 XX
 PR 11-APR-2000; 2000FR-00004629.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Buchrieser C, Frangeul L, Couve E, Rusnick C, Fsihi H, Dehoux P;
 PI Dubussguet O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cobart P;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Madueno E, De Pablo B, Weiland J, Kaelest U, Entian K, Hauf J;
 PI Rose M, Voss H;
 DR WPI; 2002-010914/01.
 XX
 PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related PT polypeptides.
 XX
 PS Claim 6; SEQ ID NO 286; 192pp; French.

XX
 CC The present invention relates to the genome sequence of *Listeria monocytogenes* B2-e (see ABA0041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in *L. monocytogenes* and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of *L. monocytogenes* and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate *L. monocytogenes*-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by *L. monocytogenes* and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 Sequence 118 AA;

Query Match 51.1%; Score 304; DB 6; Length 119;
 Best Local Similarity 54.2%; Pred. No. 2.5e-28;
 Matches 64; Conservative 20; Mismatches 32; Indels 2; Gaps 1;

Query Match	48.2%	Score 287;	DB 5;	Length 118;
Best Local Similarity	50.9%	Pred. No.	2.8e-26;	
Matches	58;	Conservative	21;	Mismatches 35;
				Indels 0;
				Gaps 0;
CC	strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> , <i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences			
CC	RESULT 6			
CC	ABU32572	standard; protein; 118 AA.		
CC	ABU32572;			
CC	19-JUN-2003	(first entry)		
CC	Protein encoded by prokaryotic essential gene #18099.			
CC	Antisense; prokaryotic essential gene; cell proliferation; drug design.			
CC	Listeria monocytogenes.			
CC	WO20027183-A2.			
CC	03-OCT-2002.			
CC	21-MAR-2002;	2002WO-05009107.		
CC	21-MAR-2001;	2001US-00815242.		
CC	06-SEP-2001;	2001US-0094893.		
CC	25-OCT-2001;	2001US-034223P.		
CC	08-FEB-2002;	2002US-00072851.		
CC	06-MAR-2002;	2002US-0362699P.		
CC	(ELIT-) ELTRA PHARM INC.			
CC	Wang L, Zamudio C, Malone C, Hasebeck R, Ohlsen KL, Zyskind JW;			
CC	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;			
CC	WPI; 2003-029926/02.			
CC	N-PSDB; ACB36442.			
CC	New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.			
CC	Claim 25;	SEQ ID NO 60495;	176pp;	English.
CC	The invention relates to an isolated nucleic acid comprising any one of the nucleic acid sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of			
CC	RESULT 7			
CC	ABP39429	standard; protein; 124 AA.		
CC	ABP39429;			
CC	AC			
CC	ABP39429;			
CC	XX			
CC	DT	24-JUL-2002	(first entry)	
CC	XX	Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4274.		
CC	XX	Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; KW antibacterial; gene therapy.		
CC	XX	Staphylococcus epidermidis.		
CC	OS			
CC	XX	US6380370-B1.		
CC	PN			
CC	PD	30-APR-2002.		
CC	XX			
CC	PF	13-AUG-1998;	98US-00134001.	
CC	XX			
CC	PR	14-AUG-1997;	97US-0055779P.	
CC	XX			
CC	PR	08-NOV-1997;	97US-0064964P.	
CC	XX			
CC	PA	(GENO-) GENOME THERAPEUTICS CORP.		
CC	XX			
CC	PT	Doucette-Stamm LA, Bush D;		
CC	DR	WPI; 2002-381255/41.		
CC	XX	N-PSDB; ABN91974.		
CC	PT	Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections.		
CC	XX			
CC	DS	Disclosure; SEQ ID NO 4274;	267pp;	English.
CC	XX			
CC	ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The <i>S. epidermidis</i> sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly <i>S. epidermidis</i> infections. The sequences can be used to screen for compounds able to interfere with the <i>S. epidermidis</i> life cycle or inhibit <i>S. epidermidis</i> infection. N.B. The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from the USPRO web site			

xx
 SQ Sequence 124 AA:
 Query Match 47.3%; Score 281.5; DB 5; Length 124;
 Best Local Similarity 51.3%; Pred. No. 1.4e-25;
 Matches 61; Conservative 20; Mismatches 29; Indels 9; Gaps 4;
 YYGIGDITELKRRIASMAGRQGRPAERILT--RSELDDQYVLESERKRNNEFLAGRAKEA 58
 10 YGIGDITELKRRIASMAGRQGRPAERILT--RSELDDQYVLESERKRNNEFLAGRAKEA 66
 Ps 59 FSKAFTGIGRQLSFDIEIRKDQMGKPYIICTKLSQAAVHSWSTHTKEYAAQWIER 117
 Db 67 FSKALGTGIGLKSVSFQDINCYNDALGKP--CIDYPGFYHVSITHTENAMSQVIEK 122

RESULT 8
 ADS04560
 ID ADS04560 standard; protein; 124 AA.
 AC ADS04560;
 DT 04-NOV-2004 (first entry)
 XX
 DE Staphylococcus epidermidis polypeptide seqid 3855.
 XX
 KW antibacterial; vaccine; antisense therapy; *Staphylococcus epidermidis*;
 KW recombinant expression vector; infection; computer readable medium;
 KW computer based system.
 XX
 OS *Staphylococcus epidermidis*.
 XX
 US2004147734-A1.
 PP 01-DEC-2003; 2003US-00724972.
 PR 08-NOV-1997; 97US-0064964P.
 PR 13-AUG-1998; 98US-00134001.
 PR 29-NOV-1999; 99US-00450969.
 XX
 PA (DOUCETTE) DOUCETTE-STAMM L.
 PA (BUSH) BUSH D.
 PT Doucette-Stamm L., Bush D;
 XX
 DR WPI; 2004-580138/56.
 DR N-PSDB; ADS00788.
 XX
 PT New isolated polypeptide and encoding nucleic acid derived from
 PT treating an *S. epidermidis* bacterial infection.
 PS Claim 17; SEQ ID NO 3855; 741pp; English.

The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772), and encoding an *Staphylococcus epidermidis* polypeptide with any given in the specification. Also described are: a recombinant expression vector; a cell comprising a recombinant expression vector of (1); producing an *S. epidermidis* polypeptide; an isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an *S. epidermidis* infection, comprising a nucleic acid cited above and a carrier; treating a subject for *S. epidermidis* infection; a recombinant or substantially pure preparation of an *S. epidermidis* polypeptide or its fragment; a vaccine composition for prevention or treatment of an *S. epidermidis* infection; detecting the presence of a *Staphylococcus* nucleic acid in a sample; a computer readable medium having recorded in it the nucleotide sequences with SEQ ID NO: 1-3772 or its fragments; a computer based system for identifying fragments of the *Staphylococcus* genome of

CC commercial importance; a computer based system for identifying fragments of the *Staphylococcus* plasmids of commercial importance; identifying commercially important nucleic acid fragments of the *Staphylococcus* genome and/or plasmids; and identifying an expression modulating fragment of the *Staphylococcus* genome and/or plasmids. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of an *Staphylococcal* bacterial infection. This is the amino acid sequence of a *S. epidermidis* protein of the invention.

xx
 SQ Sequence 124 AA:
 Query Match 47.3%; Score 281.5; DB 8; Length 124;
 Best Local Similarity 51.3%; Pred. No. 1.4e-25;
 Matches 61; Conservative 20; Mismatches 29; Indels 9; Gaps 4;
 YYGIGDITELKRRIASMAGRQGRPAERILT--RSELDDQYVLESERKRNNEFLAGRAKEA 58
 10 YGIGDITELKRRIASMAGRQGRPAERILT--RSELDDQYVLESERKRNNEFLAGRAKEA 66
 Ps 59 FSKAFTGIGRQLSFDIEIRKDQMGKPYIICTKLSQAAVHSWSTHTKEYAAQWIER 117
 Db 67 FSKALGTGIGLKSVSFQDINCYNDALGKP--CIDYPGFYHVSITHTENAMSQVIEK 122

RESULT 9
 ABU42933
 ID ABU42933 standard; protein; 117 AA.
 AC ABU42933;
 AC ABU42933;
 DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #28460.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Staphylococcus epidermidis*.
 XX
 WO20027183-A2.
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-0094993.
 PR 25-OCT-2001; 2001US-034923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Wang L., Zamudio C., Malone C., Haselebeck R., Ohisen Ku., Zyskind JW;
 PI Wall D., Trawick JD., Carr GJ., Yamamoto R., Forsyth RA., Xu HH;
 DR WPI; 2003-029956/02.
 DR N-PSDB; ACR46803.

XX
 PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 70857; 176pp; English.

XX
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 117 AA;

RESULT 10

Query Match	Score	DB	Length
Best Local Similarity	47.0%	6	117
Matches	51.3%	Pred.	No. 2.2e-25;
61; Conservative	19;	Mismatches	30;
Indels	9;	Gaps	
QY	2 YGIGLDITELKRIASMACRQKPARERIT--RSELDDQYIYESEKKRNKEFLAGRAKEA 58		
3 YGIGLDITELKRIASMACRQKPARERIT--RSELDDQYIYESEKKRNKEFLAGRAKEA 59			
DB	59 FSKAGFTGTGROLSPFDTTEIRKDKONGKREYVITCKLQSAAVHVSITMKKEYAAQVTER 117		
QY	60 FSKAGLGIGLGKSVSQDINCYNDALGR--CIDYPGFTYHSITTENIAMSQILEK 115		
DB			

ABU43645 standard; protein; 119 AA.

AC ABU43645;

XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #29172.

XX OS *Staphylococcus haemolyticus*.

XX PN WO20027183-A2.

XX WO20027183-A2.

XX PD 03-OCT-2002.

XX PR 21-MAR-2002; 2002WO-US0009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-0094893.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELTRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zvaskina JW, Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PADB; ACA47515.

PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation or to isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 71569; 1766pp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which the proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) Profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs; or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
 CC ftp://wipo.int/Pub/published_pat_sequences
 CC
 XX Sequence 119 AA;
 SQ

Query Match	Local Similarity	Score	DB	Length
Best	50.0%	278.5	6	119
Matches	59;	Pred. No.	3e-25;	
	Conservative			
	Mismatches			
	59;			
	Indels			
	5;			
	Gaps			
	3;			

QY 2 YGIGDITELKRRIASWAGRK-REFERILRSELQOYEL-SEKRNKEFLAGREFAKEAF 59
 DB :|||: :| :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 3 HGIGIDLIEDIRRIKAFEROKDKLVRLTQBEEQPHSFKSEKRKFKEFLSGRFATKEAF 62

QY 60 SKAFTGIGRQLSDFDIEIRKDQNGSKPYIICKLS-QAVHISITHTKEYAAQVIER 117
 DB :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 63 SKAFTGIGRQLSDFDIEIRKDQNGSKPYIICKLS-QAVHISITHTKEYAAQVIER 117

RESULT 11
 ABR83238
 ID ABR83238 standard; protein; 119 AA.
 XX
 AC ABR83238;
 XX
 DT 30-SEP-2003 (first entry)
 XX
 DE S. aureus acyl carrier protein synthase acps protein SEQ ID NO:32.
 XX
 KW Crystallised recombinant polypeptide; *Staphylococcus aureus*; vaccine;
 KW *Streptococcus pneumoniae*; *Helicobacter pylori*; *Pseudomonas aeruginosa*;
 KW membrane biosynthesis; crystal form; antibacterial; crystal structure;
 KW immunological response; vaccination; ftsZ; fabZ; fabG; acps; murD; murC;
 KW fabH; tagD; obg.
 OS *Staphylococcus aureus*.
 XX
 PN WO2003027139-A2.

PD	03-APR-2003.	XX	DT	20-NOV-2003 (first entry)	
PF	24-SEP-2002; 2002WO-CA001443.	XX	DR	Staphylococcus aureus protein #1039.	
PR	24-SEP-2001; 2001US-032449P.	XX	KW	Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target.	
PR	24-SEP-2001; 2001US-0324504P.	XX	OS	Staphylococcus aureus.	
PR	01-OCT-2001; 2001US-0324269P.	XX	PN	WO200294868-A2.	
PR	03-OCT-2001; 2001US-0324887P.	XX	PD	28-NOV-2002.	
PR	24-OCT-2001; 2001US-0334560P.	XX	PP	27-MAR-2002; 2002WO-1B002637.	
PR	24-OCT-2001; 2001US-0334471P.	XX	PR	27-MAR-2001; 2001US-0343000P.	
PR	26-OCT-2001; 2001US-0343000P.	XX	PR	27-MAR-2001; 2001US-0343002P.	
PR	26-OCT-2001; 2001US-0343002P.	XX	PR	27-MAR-2001; 2001US-0343007P.	
PR	18-DEC-2001; 2001US-0343767P.	XX	XX	27-MAR-2001; 2001US-0343946P.	
PR	21-DEC-2001; 2001US-034307P.	XX	PA	(AFFI-) AFFINITY PHARM INC.	
XX		XX	PA	(CHIR-) CHIRON SPA.	
PA		XX	PA	N-PSB; ACF06197.	
XX		XX	PI	Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B, Mansouri K;	
PT	Canadian V, Domagala M, Houston S, Kanagarajah D, Li Q, Mansouri K;	XX	PI	McDonald M, Necakova S, Ng I, Pinder B, Sheldrick B, Vallee F;	
PT	McDonald M, Necakova S, Ng I, Pinder B, Sheldrick B, Vallee F;	XX	PI	Violà C, Wrezel O;	
XX		XX	PS	WPI; 2003-441048/41.	
DR		XX	PS	N-PSB; ACF06197.	
XX		XX	PT	Novel crystallized recombinant polypeptides from <i>Staphylococcus aureus</i> , <i>S. aureus</i> , <i>Streptococcus pneumoniae</i> and <i>Helicobacter pylori</i> and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria.	
CC	The present invention describes a crystallised recombinant polypeptide (I) comprising amino acid sequence of polypeptides from <i>Staphylococcus aureus</i> , <i>Streptococcus pneumoniae</i> , <i>Helicobacter pylori</i> and <i>Pseudomonas aeruginosa</i> , and streptococci which are involved in membrane biosynthesis, or amino acid sequences having at least 90 % identity with the polypeptide sequence, where the polypeptide is in crystal form. (I) has antibacterial activity and can be used in vaccines. (I) is useful for designing a modulator for the prevention or treatment of <i>S. aureus</i> , <i>H. pylori</i> , <i>S. pneumoniae</i> , and <i>P. aeruginosa</i> -related disease or disorder. (I) is also useful for identifying small molecules that bind to a recombinant polypeptide. The structural and functional information of (I) aid in the discovery and design of therapeutic and diagnostic molecules. The crystal structure is useful to make a structural or computer model of the polypeptide, complex or its portion. (I) can be used for inducing an immunological response in an individual and as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. ACF06185 to ACF0632 and ABR83203 to ABR8333 represent sequences used in the exemplification of the present invention	XX	PS	Claim 1; SEQ ID NO 2078; 49PP; English.	
CC	Sequence 119 AA;	XX	PT	New <i>Staphylococcus aureus</i> protein, useful as a vaccine for treating or preventing <i>Staphylococcal</i> infection, specifically an infection caused by <i>S. aureus</i> , e.g. sepsis.	
CC	Sequence 119 AA;	XX	PT	Preventing <i>Staphylococcal</i> infection, specifically an infection caused by <i>S. aureus</i> , e.g. sepsis.	
CC	Sequence 119 AA;	XX	PS	WPI; 2003-120786/11.	
CC	Sequence 119 AA;	XX	DR	N-PSB; ACF73359.	
CC	Sequence 119 AA;	XX	PA	(CHIR-) CHIRON SPA.	
CC	Sequence 119 AA;	XX	PA	N-PSB; ACF73359.	
CC	Sequence 119 AA;	XX	PT	The invention relates to novel genes and encoded proteins from <i>Staphylococcus aureus</i> . A composition comprising the <i>S. aureus</i> protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to <i>Staphylococcus</i> bacteria, specifically an infection caused by <i>S. aureus</i> . The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel <i>S. aureus</i> proteins of the invention	
CC	Sequence 119 AA;	XX	PS	Sequence 119 AA;	
CC	Sequence 119 AA;	XX	PT	Query Match 46.7%; Score 278; DB 6; length 119; Best Local Similarity 46.7%; Pred. No. 3.5e-25; Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2;	
CC	Sequence 119 AA;	XX	PS	Query Match 46.7%; Score 278; DB 6; length 119; Best Local Similarity 48.7%; Pred. No. 3.5e-25; Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2;	
OY	2 YGIGDITTELKRKIASMAGRKRFRAERLTLRSELDQYVELS-EKRRNKFALGRFAAKEAFS 60	OY	2 YGIGDITTELKRKIASMAGRKRFRAERLTLRSELDQYVELS-EKRRNKFALGRFAAKEAFS 60	Db	3 HGIQVLDLEIDRQLAISKOPKLVERILTKNQHFKNNFTHEQRKIEFLAGRFAKEAFS 62
OY	3 HGIQVLDLEIDRQLAISKOPKLVERILTKNQHFKNNFTHEQRKIEFLAGRFAKEAFS 62	OY	3 HGIQVLDLEIDRQLAISKOPKLVERILTKNQHFKNNFTHEQRKIEFLAGRFAKEAFS 62	Db	61 KAGFTGIGRQSPDQEIRKONGKYIICLKLSQAQVHSITHKEYAAQVIER 117
Db	61 KAGFTGIGRQSPDQEIRKONGKYIICLKLSQAQVHSITHKEYAAQVIER 117	OY	61 KAGFTGIGRQSPDQEIRKONGKYIICLKLSQAQVHSITHKEYAAQVIER 117	Db	63 KALGTGIGKHAFNFDICYNDNLBLGKPKI--DYEGETIVHVSISHTEHYAMSQVLEK 116
RESULT 12	ABM71799	RESULT 13	AC	ABM71799 standard; protein; 119 AA.	
ID	ABM71799	ID	AC	AAU33845; 14-FEB-2002 (first entry)	
XX	ABM71799	XX	DE	Staphylococcus aureus cellular proliferation protein #121.	
XX		XX	XX	Antisense; prokaryotic cellular proliferation protein; antibiotic; Staphylococcus aureus.	
AC	ABM71799;	PN	OS	W0200170955-A2.	

XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 25-OCT-2000; 2000US-025758P.
PR 27-NOV-2000; 2000US-025365P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0259308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
XX
N-PSDB; AAS51704.
PT New polynucleotides for the identification and development of
XX
PT antibiotics, comprise sequences of antisense nucleic acids.
PS Example 3; SEQ ID NO 5341; 51pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
useful for the identification of potential new targets for antibiotic
development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 119 AA;

Query Match 46.6%; Score 277; DB 4; Length 119;
Best Local Similarity 48.7%; Pred. No. 4.6e-25; Gaps 2;
Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2;

QY 2 YGIGDTEKLKRISMGKRFKAERILTRSLDQYVYES-EKKRNKEFLAGRFAKEAFS 60
Db 3 HGIGVDLIEIDRIVKLISKQPKLVERILTKNEOHKFNNFTBORKIEFLAGRFATEAFS 62

QY 61 KAFGTGIGRQSLFQDIETRKDONGKPYIICTKLSQAANAVHSINTHTKEYAAQVIER 117
Db 63 KALGTGLGKHVAFNIDCYNDSLKGPKI--DYEGLFIVHVSISHTQYAMQVULEK 116

RESULT 14
AAU36608
ID AAU36808 standard; protein; 119 AA.

AC AAU36808;
XX
DT 14-FEB-2002 (first entry)
DE Staphylococcus aureus cellular proliferation protein #978.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
antibacterial; drug design.
XX

OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PR 21-MAR-2001; 2001WO-US009180.
XX
PT 21-MAR-2000; 2000US-0191078P.
XX
PR 21-MAR-2000; 2000US-0206848P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0259308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
BA (ELIT-) ELITRA PHARM INC.
XX
PT Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
XX
N-PSDB; AAS54667.
PT New polynucleotides for the identification and development of
XX
PT antibiotics, comprise sequences of antisense nucleic acids.
PS Example 3; SEQ ID NO 12401; 51pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 119 AA;

Query Match 46.6%; Score 277; DB 4; Length 119;
Best Local Similarity 48.7%; Pred. No. 4.6e-25; Gaps 2;
Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2;

QY 2 YGIGDTEKLKRISMGKRFKAERILTRSLDQYVYES-EKKRNKEFLAGRFAKEAFS 60
Db 3 HGIGVDLIEIDRIVKLISKQPKLVERILTKNEOHKFNNFTBORKIEFLAGRFATEAFS 62

QY 61 KAFGTGIGRQSLFQDIETRKDONGKPYIICTKLSQAANAVHSINTHTKEYAAQVIER 117
Db 63 KALGTGLGKHVAFNIDCYNDSLKGPKI--DYEGLFIVHVSISHTQYAMQVULEK 116

RESULT 15
AAB14979
ID AAB14979 standard; protein; 119 AA.
XX
AC AAB14979;
XX
DT 01-DEC-2000 (first entry)
DE Staphylococcus aureus phosphopantethienyl transferase protein Acps.
XX

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

This Page Blank (uspto)

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GeneFare version 5.1.6

OM protein - protein search, using sw model

Run on:	December 21, 2005, 13:54:50 ; Search time 5.64179 Seconds
Scoring table:	BIGSUM62
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Perfect score:	US-10-717-138-1
Gapop 10.0 , Gapext 0.5	
Searched:	53982 seqs, 7132107 residues
Total number of hits satisfying chosen parameters:	53982
Minimum DB seq length:	0
Maximum DB seq length:	200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

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1: Published Applications AA New:*
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3: /cgn2_6_ptodata/2/pubpaa/US07_NEW_PUB_PEP:*
4: /cgn2_6_ptodata/2/pubpaa/PCT_NEW_PUB_PEP:*
5: /cgn2_6_ptodata/2/pubpaa/US09_NEW_PUB_PEP:*
6: /cgn2_6_ptodata/2/pubpaa/US10_NEW_PUB_PEP:*
7: /cgn2_6_ptodata/2/pubpaa/US11_NEW_PUB_PEP:*
8: /cgn2_6_ptodata/2/pubpaa/US60_NEW_PUB_PEP:*

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Result

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1	217	54.7	76	6 US-10-467-657-4016	Sequence 4016, Ap
2	217	54.7	78	6 US-10-467-657-3996	Sequence 3996, Ap
3	217	54.7	78	6 US-10-467-657-7044	Sequence 7044, Ap
4	135	34.0	178	6 US-10-821-234-1552	Sequence 1052, Ap
5	94.5	23.8	2910	7 US-11-087-100-2	Sequence 2, Appli
6	94.5	23.8	2910	7 US-11-087-084-2	Sequence 2, Appli
7	94.5	23.8	2910	7 US-11-087-085-2	Sequence 2, Appli
8	91.5	23.0	86	7 US-11-087-013	Sequence 13, Appli
9	91.5	23.0	86	7 US-11-087-084-13	Sequence 13, Appli
10	91.5	23.0	86	7 US-11-087-085-13	Sequence 13, Appli
11	73.5	18.5	371	6 US-10-467-662B-41	Sequence 214, Appli
12	68	17.1	697	7 US-11-074-176-214	Sequence 214, Appli
13	65.5	16.5	412	7 US-11-082-389-96	Sequence 96, Appli
14	62.5	15.7	642	6 US-10-467-657-5000	Sequence 5900, Ap
15	62	15.6	1061	7 US-11-059-814-18	Sequence 18, Appli
16	61.5	15.6	530	6 US-10-858-130-67	Sequence 67, Appli
17	61	15.4	1001	6 US-10-467-962B-81	Sequence 81, Appli
18	60	15.1	327	7 US-11-129-143-91	Sequence 91, Appli
19	60	15.1	1766	7 US-11-075-185-10	Sequence 10, Appli
20	59.5	15.0	188	7 US-11-194-246-292	Sequence 292, Appli
21	59	14.9	122	7 US-11-793-626-564	Sequence 564, Appli
22	59	14.9	128	7 US-11-105-894-4	Sequence 4, Appli
23	59	14.9	274	6 US-10-467-657-2140	Sequence 2140, Appli
24	58.5	14.9	449	6 US-10-485-517-272	Sequence 272, Appli
25	58.5	14.7	269	6 US-10-793-626-2472	Sequence 2472, Appli

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

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Sequence 1, App
Sequence 11, App
Sequence 2, App
Sequence 2730, App
Sequence 4, App
Sequence 45, App
Sequence 143, App
Sequence 147, App
Sequence 141, App
Sequence 2296, App
Sequence 6816, App
Sequence 9, Appli
Sequence 3020, App
Sequence 292, App
Sequence 2058, App
Sequence 2, Appli
Sequence 1, Appli
Sequence 1573, App
Sequence 1506, App
Sequence 2, Appli
Sequence 10, Appli
Sequence 1278, App

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FILE REFERENCE: ; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3996
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-3996

RESULT 3
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Best Local Similarity 66.2%; Pred. No. 9.4e-16;
Matches 45; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
Match No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: RONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MAGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEAR ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7044
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-7044

Query Match 54.7%; Score 217; DB 6; Length 78;
Best Local Similarity 66.2%; Pred. No. 9.4e-16;
Matches 45; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
Match No. US-10-467-657-7044
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stacie-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; RESULT 4
US-10-821-234-1052
; Sequence 1052, Application US/10821234
; Publication No. US2005025114A1

RESULT 5
Query Match 34.0%; Score 135; DB 6; Length 178;
Best Local Similarity 37.5%; Pred. No. 3.7e-07;
Matches 30; Conservative 17; Mismatches 33; Indels 0; Gaps 0;
Match No. US20050266440A1
; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Flatt, James
; APPLICANT: Kuner, Jerry
; TITLE OF INVENTION: System and Uses Thereof
; FILE REFERENCE: 2997-29
; CURRENT APPLICATION NUMBER: US/11/087,100
; CURRENT FILING DATE: 2005-03-21
; PRIOR APPLICATION NUMBER: 09/231,899
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/284,066
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/298,796
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/323,269
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2
; LENGTH: 2910
; TYPE: PRT
; ORGANISM: Schizophytrium sp.
; US-11-087-100-2

Query Match 23.8%; Score 94.5; DB 7; Length 2910;
Best Local Similarity 31.3%; Pred. No. 0.12;
Matches 26; Conservative 18; Mismatches 26; Indels 13; Gaps 3;
Match No. US-11-087-100-2
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stacie-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; RESULT 6
US-11-087-084-2
; Sequence 2, Application US/11087084
; Publication No. US20050273883A1


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Page 6

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; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Flatt, James
; APPLICANT: Kuner, Jerry
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
; TITLE OF INVENTION: System and Uses Thereof
FILE REFERENCE: 2997-29
CURRENT APPLICATION NUMBER: US/11/087,084
CURRENT FILING DATE: 2005-03-21
PRIORITY APPLICATION NUMBER: 09/231,899
PRIORITY FILING DATE: 1999-01-14
PRIORITY APPLICATION NUMBER: 60/284,066
PRIORITY FILING DATE: 2001-04-16
PRIORITY APPLICATION NUMBER: 60/298,796
PRIORITY FILING DATE: 2001-06-15
PRIORITY APPLICATION NUMBER: 60/323,269
PRIORITY FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.3
ORGANISM: Schizochytrium sp.
US-11-087-084-2

Query Match 23.8%; Score 94.5; DB 7; Length 2910;
Best Local Similarity 31.3%; Pred. No. 0.12; Mismatches 26; Indels 13; Gaps 3;
Matches 26; Conservative 18; Mismatches 26; Indels 13; Gaps 3;
QY 2 PLGSATLERTVTKIVDRIGVD-----EADVKLEASFKEFDLGDSLDVVELVNELED 53
Db 1114 PAVSNELLEKAETVWMEVLAAKTGYETDMIEADMLEET---ELGIDSIRKVEILSEVOA 1169
QY 54 BFDMEISDEDA-EKIAVGDVN 75
Db 1170 MLNVEAKDVKDALSRTTVGEVWN 1192

RESULT 7
US-11-087-085-2

Query Match 23.8%; Score 94.5; DB 7; Length 2910;
Best Local Similarity 31.3%; Pred. No. 0.12; Mismatches 26; Indels 13; Gaps 3;
Matches 26; Conservative 18; Mismatches 26; Indels 13; Gaps 3;
QY 2 PLGSATLERTVTKIVDRIGVD-----EADVKLEASFKEFDLGDSLDVVELVNELED 53
Db 1114 PAVSNELLEKAETVWMEVLAAKTGYETDMIEADMLEET---ELGIDSIRKVEILSEVOA 1169
QY 54 BFDMEISDEDA-EKIAVGDVN 75
Db 1170 MLNVEAKDVKDALSRTTVGEVWN 1192

RESULT 8
US-11-087-100-13
; Sequence 13, Application US/11087100
; Publication No. US20050256640A1
; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Flatt, James
; APPLICANT: Kuner, Jerry
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
; TITLE OF INVENTION: System and Uses Thereof
FILE REFERENCE: 2997-29
CURRENT APPLICATION NUMBER: US/11/087,100
CURRENT FILING DATE: 2005-03-21
PRIORITY APPLICATION NUMBER: 09/231,899
PRIORITY FILING DATE: 1999-01-14
PRIORITY APPLICATION NUMBER: 60/284,066
PRIORITY FILING DATE: 2001-04-16
PRIORITY APPLICATION NUMBER: 60/298,796
PRIORITY FILING DATE: 2001-06-15
PRIORITY APPLICATION NUMBER: 60/323,269
PRIORITY FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.3
SEQ ID NO 13
QY 57 MEISDEDA-EKIAVGDVN 75
Db 59 VEAKDVKDALSRTTVGEVWN 78

RESULT 9
US-11-087-084-13
; Sequence 13, Application US/11087084
; Publication No. US2005273803A1
; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Flatt, James
; APPLICANT: Kuner, Jerry
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
; TITLE OF INVENTION: System and Uses Thereof
FILE REFERENCE: 2997-29
CURRENT APPLICATION NUMBER: US/11/087,084
CURRENT FILING DATE: 2005-03-21
PRIORITY APPLICATION NUMBER: 09/231,899
PRIORITY FILING DATE: 1999-01-14
PRIORITY APPLICATION NUMBER: 60/284,066
PRIORITY FILING DATE: 2001-04-16
PRIORITY APPLICATION NUMBER: 60/298,796
PRIORITY FILING DATE: 2001-06-15
PRIORITY APPLICATION NUMBER: 60/323,269
PRIORITY FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.3
SEQ ID NO 2
LENGTH: 2910
TYPE: PRT
ORGANISM: Schizochytrium sp.
US-11-087-085-2

Query Match 23.8%; Score 94.5; DB 7; Length 2910;
Best Local Similarity 31.3%; Pred. No. 0.12; Mismatches 26; Indels 13; Gaps 3;
Matches 26; Conservative 18; Mismatches 26; Indels 13; Gaps 3;
QY 54 BFDMEISDEDA-EKIAVGDVN 75
Db 1114 PAVSNELLEKAETVWMEVLAAKTGYETDMIEADMLEET---ELGIDSIRKVEILSEVOA 1169
QY 54 EPDMEISDEDA-EKIAVGDVN 75
Db 1170 MLNVEAKDVKDALSRTTVGEVWN 1192

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; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 13
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Schizochytrium sp.
; US-11-087-084-13

Query Match 23.0%; Score 91.5; DB 7; Length 86;
Best Local Similarity 31.2%; Pred. No. 0.0033; Matches 25; Conservative 18; Mismatches 24; Indels 13; Gaps 3;
Qy 5 SADTLERVTKILVDRLGVD-----EADVKLEASFKEDEDIGADSLSLUVVLMELDEFD 56
Db 3 SNELLEKAETVVMEVLAKTGVTDMLEADMLET---EGLDSIKRVEILSEVOAMLN 58
Qy 57 METSDEDA-EKIAVTGDAVN 75
Db 59 VEAKDVDAISRTTVGEVN 78

RESULT 10
US-11-087-085-13
Sequence 13, Application US/11087/085
Publication No. US20050273884A1
GENERAL INFORMATION:
APPLICANT: Metz, James
APPLICANT: Barclay, William
APPLICANT: Flatt, James
APPLICANT: Kuner, Jerry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
FILE REFERENCE: 2997-29
CURRENT APPLICATION NUMBER: US/11/087, 085
CURRENT FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: 09/231, 899
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/284, 066
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/298, 796
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/323, 269
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 13
LENGTH: 86
TYPE: PRT
ORGANISM: Schizochytrium sp.
US-11-087-085-13

Query Match 23.0%; Score 91.5; DB 7; Length 86;
Best Local Similarity 31.2%; Pred. No. 0.0033; Matches 25; Conservative 18; Mismatches 24; Indels 13; Gaps 3;
Qy 5 SADTLERVTKILVDRLGVD-----EADVKLEASFKEDEDIGADSLSLUVVLMELDEFD 56
Db 3 SNELLEKAETVVMEVLAKTGVTDMLEADMLET---EGLDSIKRVEILSEVOAMLN 58
Qy 57 METSDEDA-EKIAVTGDAVN 75
Db 59 VEAKDVDAISRTTVGEVN 78

RESULT 11
US-10-467-962B-41
Sequence 41, Application US/10467962B
Publication No. US20050246784A1
GENERAL INFORMATION:
APPLICANT: Plesch, Gunnar
APPLICANT: Blau, Astrid
APPLICANT: Daeschner, Klaus

RESULT 12
US-11-074-1176-214
Sequence 214, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Stress-Related Proteins and Uses Thereof
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074, 176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551, 161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 214
LENGTH: 697
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
US-11-074-1176-214

Query Match 17.1%; Score 68; DB 7; Length 697;
Best Local Similarity 27.6%; Pred. No. 9.2; Matches 21; Conservative 14; Mismatches 27; Indels 14; Gaps 2;
Qy 2 PIGSADTLERVTKILVDRLGVD-----VDRLGVDADVKLEASFKEDEDIGADSLSLUVVLMELDEFD 53
Db 167 PIGSADTLERVTKILVDRLGVD-----VDRLGVDADVKLEASFKEDEDIGADSLSLUVVLMELDEFD 226
Qy 54 BF-----DMEISDED 63
Db 227 NIMEKYLGGERBISNDE 242

RESULT 13
US-11-082-389-96
Sequence 96, Application US/11082389
Publication No. US20050244935A1
GENERAL INFORMATION:
APPLICANT: Pompeius, Markus
APPLICANT: Kroger, Burkhard

```

APPLICANT: Schröder, Hartwig
 APPLICANT: Zelder, Oskar
 APPLICANT: Haberhauer, Gregor
 TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT
 FILE REFERENCE: BGI-131CPCN
 CURRENT APPLICATION NUMBER: US/11/082,389
 CURRENT FILING DATE: 2005-03-16
 PRIOR APPLICATION NUMBER: US 09/603024
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 60/141031
 PRIOR FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: US 60/143262
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: US 60/151281
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19930487-4
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: DE 19930489-0
 PRIOR FILING DATE: 1999-07-01
 PRIOR APPLICATION NUMBER: DE 19931549-3
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19931550-7
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19932134-5
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19941379-7
 PRIOR FILING DATE: 1999-08-31
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 446
 SEQ ID NO 96
 LENGTH: 412
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
 US-11-082-389-96

RESULT 15
 US-11-059-814-18
 ; Sequence 18, Application US/11059814
 ; Publication No. US20050272650A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of South Florida
 ; TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell Proliferation Disorders
 ; FILE REFERENCE: US2-215PTCZ
 ; CURRENT APPLICATION NUMBER: US/11/059,814
 ; CURRENT FILING DATE: 2005-02-17
 ; PRIOR APPLICATION NUMBER: 60/521,072
 ; PRIOR FILING DATE: 2004-02-17
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 18
 ; LENGTH: 1061
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-059-814-18

Query Match 15.7%; Score 62.5; DB 6; Length 642;
 Best Local Similarity 27.7%; Pred. No. 29;
 Matches 23; Conservative 11; Mismatches 46; Indels 3; Gaps 1;

Qy 2 PIGSAMPLERVKITVDRIGV---EADVKLEASFKEIDLADSLPVLYNLEPBFDFME 58
 Db 157 PGSIATLIELIKEKICKBEIRDVVEAIDPNEVNLNLGLGHETTAPEKPSNDNSDEN 216
 Qy 59 ISDEDAEKIATVGDAVNINQQ 81
 Db 217 EDDEEEBEDABEISANLAELKQ 239

RESULT 14
 US-10-67-657-5900
 ; Sequence 5900, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Eli Isabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-03-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 5900
 ; LENGTH: 642
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 ; US-10-467-657-5900

Search completed: December 21, 2005, 14:13:51
 Job time : 6.64179 secs

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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: December 21, 2005, 13:49:45 ; Search time 89.8657 Seconds
(without alignments)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Published Applications AA_Main;*

1: /cgn2_6/ptodata/1/pubcaa/US07_PUBCOMB.pep;*
2: /cgn2_6/ptodata/1/pubcaa/US08_PUBCOMB.pep;*
3: /cgn2_6/ptodata/1/pubcaa/US09_PUBCOMB.pep;*
4: /cgn2_6/ptodata/1/pubcaa/US10A_PUBCOMB.pep;*
5: /cgn2_6/ptodata/1/pubcaa/US10B_PUBCOMB.pep;*
6: /cgn2_6/ptodata/1/pubcaa/US11_PUBCOMB.pep;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	397	100.0	81	Sequence 1, Application US-09-770-834-1
2	397	100.0	81	Sequence 1, Application US-09-770-834-1
3	397	100.0	81	Sequence 1, Application US-09-770-834-1
4	284	71.5	80	Sequence 1, Application US-09-770-834-1
5	254	64.0	77	Sequence 1, Application US-09-770-834-1
6	254	64.0	76	Sequence 1, Application US-09-770-834-1
7	249	62.7	76	Sequence 1, Application US-09-770-834-1
8	239	60.2	110	Sequence 1, Application US-09-770-834-1
9	239	59.9	77	Sequence 1, Application US-09-770-834-1
10	238	59.9	77	Sequence 1, Application US-09-770-834-1
11	238	59.9	79	Sequence 1, Application US-09-770-834-1
12	236	59.4	77	Sequence 1, Application US-09-770-834-1
13	234	58.9	77	Sequence 1, Application US-09-770-834-1
14	234	58.9	77	Sequence 1, Application US-09-770-834-1
15	234	58.9	77	Sequence 1, Application US-09-770-834-1
16	234	58.9	77	Sequence 1, Application US-09-770-834-1
17	232	58.4	73	Sequence 1, Application US-09-770-834-1
18	232	58.4	77	Sequence 1, Application US-09-770-834-1
19	227	57.2	79	Sequence 1, Application US-09-770-834-1
20	226.5	57.1	78	Sequence 1, Application US-09-770-834-1
21	226.5	56.7	104	Sequence 1, Application US-09-770-834-1
22	223.5	56.3	75	Sequence 1, Application US-09-770-834-1
23	222.5	56.0	72	Sequence 1, Application US-09-770-834-1
24	222.5	56.0	78	Sequence 1, Application US-09-770-834-1
25	222.5	56.0	79	Sequence 1, Application US-09-770-834-1
26	222.5	56.0	79	Sequence 1, Application US-09-770-834-1
27	222.5	56.0	79	Sequence 1, Application US-09-770-834-1

RESULTS

RESULT 1

US-09-770-834-1

; Sequence 1, Application US/09770834

; Subdivision No. US200302011588A1

; GENERAL INFORMATION:

; APPLICANT: Parris, Kevin

; APPLICANT: Somers, William

; APPLICANT: Tam, Amy

; APPLICANT: Lin, Laura

; APPLICANT: Stahl, Mark

; APPLICANT: Powers, Robert

; APPLICANT: Xu, Guan-Yi

; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE

; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF

; FILE REFERENCE: 2268/14

; CURRENT APPLICATION NUMBER: US/09/770-834

; CURRENT FILING DATE: 2001-10-12

; PRIORITY APPLICATION NUMBER: US 60/202,466

; PRIORITY FILING DATE: 2000-05-08

; SOFTWARE: Patentin version 3.0

; SEQ ID NO: 1

; LENGTH: 81

; TYPE: PRT

; ORGANISM: Bacillus subtilis

US-09-770-834-1

Query Match Score 100.0%; Pred. No. 2.7e-35;

Best Local Similarity 100.0%; Mismatches 0;

Matches 81; Conservative 0; Indels 0; Gaps 0;

Sequence 77373, A QY 1 GPGSAIDLTERVKIIVDRLGUDADYLKLEASPKEDGADSIDVWELVMELEDFDMIS 60

Sequence 77019, A QY 1 GPGSAIDLTERVKIIVDRLGUDADYLKLEASPKEDGADSIDVWELVMELEDFDMIS 60

Sequence 77791, A Db 1 DEDAEKATVGDANNYIQNQQ 81

Sequence 77561, A Db 1 DEDAEKATVGDANNYIQNQQ 81

Sequence 5601, A Db 1 DEDAEKATVGDANNYIQNQQ 81

Sequence 51523, A Db 1 DEDAEKATVGDANNYIQNQQ 81

Sequence 12802, A QY 61 DEDAEKATVGDANNYIQNQQ 81

Sequence 13101, A Db 61 DEDAEKATVGDANNYIQNQQ 81

Sequence 44114, A Db 61 DEDAEKATVGDANNYIQNQQ 81

Sequence 626, APP Db 61 DEDAEKATVGDANNYIQNQQ 81

Sequence 5452, AP Db 61 DEDAEKATVGDANNYIQNQQ 81

Sequence 12124, A Db 61 DEDAEKATVGDANNYIQNQQ 81

Sequence 51445, A Db 61 DEDAEKATVGDANNYIQNQQ 81

Sequence 70573, A Db 61 DEDAEKATVGDANNYIQNQQ 81

Sequence 70573, A Db 61 DEDAEKATVGDANNYIQNQQ 81

Sequence 5253, A Db 61 DEDAEKATVGDANNYIQNQQ 81

Sequence 8522, AP Db 61 DEDAEKATVGDANNYIQNQQ 81

; GENERAL INFORMATION:

; APPLICANT: Parris, Kevin

; APPLICANT: Somers, William

; APPLICANT: Tam, Amy

; APPLICANT: Lin, Laura

; APPLICANT: Stahl, Mark

Sequence 132, APP

Sequence 4732, APP

Sequence 2015, APP

Sequence 61113, APP

Sequence 9111, APP

Sequence 10628, APP

Sequence 65150, APP

Sequence 12321, APP

Sequence 65580, APP

Sequence 43145, APP

Sequence 67855, APP

Sequence 72742, APP

Sequence 75153, APP

Sequence 39, APP

Sequence 795, APP

Sequence 43145,

APPLICANT: Powers, Robert
 APPLICANT: Xu, Guan-Yi
 TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
 FILE REFERENCE: 2368/14
 CURRENT APPLICATION NUMBER: US/10/717,138
 CURRENT FILING DATE: 2003-11-19
 PRIORITY APPLICATION NUMBER: US/09/770,834
 PRIORITY FILING DATE: 2001-10-12
 NUMBER OF SEQ ID NOS: 16
 SEQ ID NO: 1
 LENGTH: 81
 TYPE: PRT
 ORGANISM: Bacillus subtilis
 US-10-717-138-1

Query Match 100.0%; Score 397; DB 4; Length 81;
 Best Local Similarity 100.0%; Pred. No. 2.7e-35; Mismatches 0; Indels 0; Gaps 0;
 Matches 81; Conservative 0; MisMatches 0;

QY 1 GPLGSATLERTKIVDRGDEADVKLEASPKEDLGADSUDVVELVMELEDFMEIS 60
 Db 1 GPLGSATLERTKIVDRGDEADVKLEASPKEDLGADSUDVVELVMELEDFMEIS 60

QY 61 DEDAEKATVGDAVNLYNQ 81
 Db 61 DEDAEKATVGDAVNLYNQ 81

QY 63 AEKIATVGDAVYIES 78
 Db 63 AEKIATVGDAVYIES 78

RESULT 3
 US-10-282-122A-46208
 ; Sequence 46208, Application US/10282122A
 ; Publication No. US2004029129A1

GENERAL INFORMATION:
 APPLICANT: Wang, Liangs
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Hasebeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20
 CURRENT APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER Of SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 60882
 LENGTH: 77
 TYPE: PRT
 ORGANISM: Listeria monocytogenes
 US-10-282-122A-60882

Query Match 71.5%; Score 284; DB 4; Length 77;

Best Local Similarity 80.8%; Pred. No. 4.1e-23; Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 6 ADTLEVKITVDRIGVEDAIVKLEASFKEDLGADSILDVVLMELDEDDEMETSDDEAS 65
Db 2 KEVLEKVTKITVDRIGVEESKVTEASFKEDLGADSILDVVLMELBDFGVELSDGAE 61

Qy 66 KIATVGDAVNVIQ 78
Db 62 NINTVGDAVKIE 74

RESULT 5
US-03-815-242-10973
; Sequence 10973, Application US/03815242
; Patent No. US2002006159A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/257,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/259,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO: 58089
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
; US-09-815-242-10973

Query Match Score 254; DB 3; Length 76;
Best Local Similarity 64.0%; Pred. No. 7.1e-20; Indels 0; Gaps 0;
Matches 52; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

RESULT 6
US-10-282-122A-58089
; Sequence 58089, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/257,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/259,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO: 58089
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
; US-10-282-122A-58089

Query Match Score 254; DB 4; Length 76;
Best Local Similarity 64.0%; Pred. No. 7.1e-20; Indels 0; Gaps 0;
Matches 52; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

RESULT 7
US-10-282-122A-67443
; Sequence 67443, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/257,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/259,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO: 58089
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
; US-10-282-122A-67443

```

; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/205,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 67443
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Pasteurella multocida
; US-10-282-122A-67443

Query Match 62.7%; Score 249; DB 4; Length 76;
Best Local Similarity 70.8%; Pred. No. 2.5e-19; Matches 51; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
Qy 10 ERVTKIIVDRGVDEADVKLEASPKEDIGASLDVVELVMISLEDMEISDDEAKIAT 69
Db 5 ERVVKIIVVEQLGKVEDKPSFVDSLTDVLMALEEFDFIPDEEAKITT 64
Qy 70 VGDAVNYYQ 81
Db 65 WQSADIVVNQQ 76

RESULT 8
US-10-282-122A-77373
; Sequence 77373, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianggu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant
; APPLICANT: Yamanoto, Robert
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Forester, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 77373
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Vibrio cholerae
; US-10-282-122A-77373

Query Match 60.2%; Score 2339; DB 4; Length 110;
Best Local Similarity 72.1%; Pred. No. 4.7e-18; Matches 49; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
Qy 10 ERVTKIIVDRGVDEADVKLEASPKEDIGASLDVVELVMISLEDMEISDDEAKIAT 69
Db 38 ERVVKIIVVEQLGKVEDKPSFVDSLTDVLMALEEFDFIPDEEAKITT 97
Qy 70 VGDAVNYY 77
Db 98 WQAIDIVY 105

RESULT 9
US-10-282-122A-70919
; Sequence 70919, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianggu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant
; APPLICANT: Yamanoto, Robert
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Forester, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-09-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 70919
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Vibrio cholerae
; US-10-282-122A-70919

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US-10-282-122A-71791

Query Match 59.9%; Score 238; DB 4; Length 77;
Best Local Similarity 67.1%; Pred. No. 3.8e-18;
Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 7 DTILERVTKIVDRLGVEDADVKLEASPKEDIGADSIDVULMELDEFDMEISDAEK 66
Db 2 ENFDKVVDIUDRLGVADKVTEDASFKDDIGADSIDIAELMELDEFGTEIPDEEAEK 61

QY 67 INTVGDAVNYTN 79

Db 62 INTVGDAVNTINS 74

RESULT 10

US-10-282-122A-71791

; Sequence 71791, Application US/10282122A
; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-10

; PRIOR APPLICATION NUMBER: 09/450,969

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: 09/134,001

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 7544

; SEQ ID NO: 5601

; LENGTH: 79

; TYPE: PRT

; ORGANISM: S. epidermidis

US-10-724-972A-5601

Query Match 59.9%; Score 238; DB 4; Length 79;
Best Local Similarity 67.1%; Pred. No. 4e-18; Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 7 DTILERVTKIVDRLGVEDADVKLEASPKEDIGADSIDVULMELDEFDMEISDAEK 66
Db 4 ENFDKVVDIUDRLGVADKVTEDASFKDDIGADSIDIAELMELDEFGTEIPDEEAEK 63

QY 67 INTVGDAVNYTN 79

Db 64 INTVGDAVNTINS 76

RESULT 12

US-10-282-122A-51523

; Sequence 51523, Application US/10282122A
; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 71791

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Staphylococcus haemolyticus

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FILE REFERENCE: ELITRA_034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-00
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/205,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 51523
LENGTH: 77
TYPE: PRT
ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51523
Query Match 59.4%; Score 236; DB 4; Length 77;
Best Local Similarity 60.9%; Pred. No. 6e-18; Matches 42; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
Qy 10 ERVTKIIVDRUGDEAVKLEASPKEDLGASLDLVELVLMELDEDMEISDEDAEK 69
Db 4 EKVKDIIADQGIDATBKKMSESSFFDLGASLDLVELMLAMEERDIEMPDEAKVSS 63
Qy 70 VGDAVNVIQ 78
Db 64 VGDVNVYIK 72
RESULT 13
US-09-815-242-12802
Sequence 12802, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlson, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA_011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/205,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO: 13101
LENGTH: 77
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13101
Query Match 58.9%; Score 234; DB 3; Length 77;
Best Local Similarity 65.8%; Pred. No. 1e-17; Matches 48; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
Qy 7 DTLERVTKIIVDRUGDEAVKLEASPKEDLGASLDLVELVLMELDEDMEISDEDAEK 66
Db 2 ENFDKRDIIIVDRUGDADQGIDATBKKMSESSFFDLGASLDLVELMLAMEERDIEMPDEAEK 61

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RESULT 15
US-10-282-122A-44414
Sequence 44414, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hasselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Travick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forryth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: BLITRA.034A
CURRENT APPLICATION NUMBER: US10/282,122A
PRIORITY FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: 60/205,848
PRIORITY FILING DATE: 2000-03-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SEQ ID NO 44414
SOFTWARE: PatentIn version 3.1
LENGTH: 77
TYPE: PRT
ORGANISM: *Staphylococcus aureus*
US-10-282-122A-44414
Query Match 58.9%; Score 234; DB 4; Length 77;
Best Local Similarity 65.8%; Pred. No. 1e-17; Mismatches 0; Gaps 0
Matches 48; Conservative 9; MisMatches 16; Indels 0;
QY 7 DTLEVRVKIIVDRGIVBDAVDKLEASFKEDLGADSLDVELVMELEDFDMEISDEAK 66
Db : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2 ENFDKVKDIIIVRGLGVADKVTEASFDLGDAGSDIAELVMELEDFGTERPDEEAK 61
QY 67 IATVGDAVNYION 79
Db 62 INTVGDAVKFINS 74

Search completed: December 21, 2005, 14:13:31
Job time : 90.8657 SECS

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 OM protein - protein search, using sw model
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 (without alignments)
 251.785 Million cell updates/sec

SUMMARIES

processing : Minimum Match 0%
 Maximum Match 100%
 Patent No. 6684162
 Listing first 45 summaries

GENERAL INFORMATION:

APPLICANT: Parrish, Kevin
APPLICANT: Somers, William
APPLICANT: Tam, Amy
APPLICANT: Lin, Laura
APPLICANT: Stahl, Mark
APPLICANT: Powers, Robert
APPLICANT: Xu, Guan-Yi
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
TITLE OF INVENTION: / O B. SUBTILIS ACP, AND USES THEREOF
FILE REFERENCE: 236B14
CURRENT APPLICATION NUMBER: US 09/770,834
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/202,466

Sequence I, Application US/09/770,834
 Issued Patents AA: *

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep: *
 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep: *
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep: *
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep: *
 6: /cgn2_6/ptodata/1/iaa/backfilles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064, 964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055, 779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 4809
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-03-134-001C-4809

Query Match      59.9%; Score 238; DB 2; Length 79;
Best Local Similarity 67.1%; Pred. No. 3.1e-21; Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
Qy    7 DPLERVKIIVDVLGKDEADVKLEASFKEDGADSIDVWLMELDEFDMEISDAEK 66
Db    4 ENFDKVDIIVDVLGKDAKVTEDASFDDLGADSDLIDIAELJWMELEDFRGTEIPDEBAAK 63
Qy    67 IATVGDVNLYQN 79
Db    64 INTVGDAVKNYS 76

RESULT 3
US-10-089-019-26
; Sequence 26, Application US/10089019
; Patent No. 6931729
; GENERAL INFORMATION:
; APPLICANT: DEWOLF, WALTER E. JR
; APPLICANT: KALLENDER, HOWARD
; TITLE OF INVENTION: METHODS FOR MAKING AND USING FATTY ACID
; TITLE OF INVENTION: SYNTHESIS PATHWAY REAGENTS
; FILE REFERENCE: GM50068
; CURRENT APPLICATION NUMBER: US /10/089, 019
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/US00/29451
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/161, 775
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 26
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-089-019-26

Query Match      58.9%; Score 234; DB 2; Length 77;
Best Local Similarity 65.8%; Pred. No. 9e-21; Matches 48; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
Qy    7 DPLERVKIIVDVLGKDEADVKLEASFKEDGADSIDVWLMELDEFDMEISDAEK 66
Db    2 ENFDKVDIIVDVLGKDAKVTEDASFDDLGADSDLIDIAELJWMELEDFRGTEIPDEBAAK 61
Qy    67 IATVGDVNLYQN 79
Db    62 INTVGDAVKNFINS 74

RESULT 4
US-09-543-681A-7956
; Sequence 4, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A

; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128, 706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO: 7956
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-7956

Query Match      56.7%; Score 225; DB 2; Length 94;
Best Local Similarity 65.7%; Pred. No. 1.4e-19; Matches 46; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
Qy    10 ERVTKIIVDVLGKDEADVKLEASFKEDGADSIDVWLMELDEFDMEISDAEKAT 69
Db    22 ERVKIIVDVLGKKEEVNSASFDDLGADSLDTVELVMALEBEFDIEPDEBAAKTT 81
Qy    70 VGDVNLYQN 79
Db    82 VQAIDYVEN 91

RESULT 5
US-09-902-540-14560
; Sequence 14560, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinke, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902, 540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217, 883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO: 14560
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-14560

Query Match      56.0%; Score 222.5; DB 2; Length 80;
Best Local Similarity 59.0%; Pred. No. 2.3e-19; Matches 46; Conservative 14; Mismatches 17; Indels 1; Gaps 1;
Qy    5 SADTLE-RVTKIIVDVLGKDEADVKLEASFKEDGADSIDVWLMELDEFDMEISDAEK 63
Db    2 STSITPEAKVSIIAQOLGVGEDEIKPPESSFTIEDLGADSIDVWLMANEEFEVEIPDE 61
Qy    64 AEKIAITVGDVNLYQNQ 81
Db    62 AENIKTNDAVSYNTH 79

RESULT 6
US-03-770-834-15
; Sequence 15, Application US/097700834
; Patent No. 6684162
; GENERAL INFORMATION:
; APPLICANT: Parrish, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14

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CURRENT APPLICATION NUMBER: US/09/770,834
 CURRENT FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: US 60/202,466
 PRIOR FILING DATE: 2000-05-08
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 15
 LENGTH: 77
 TYPE: PRT
 ORGANISM: Escherichia coli

US-09-770,834-15

Query Match 54.2%; Score 215; DB 2; Length 77;
 Best Local Similarity 63.9%; Pred. No. 1.7e-18;
 Matches 46; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 10 ERVTKITIVDRIGVEDADVKLEASFKEFDLGASLDVVELVMELEDFDMEISDEDAEKIAT 69
 Db 5 ERVKKITGEOLGVQKQEVTNNASFVDLGASLDTVELVMALEEEFTEIPDEBAEKITT 64

Qy 70 VGDAVNYIQNQ 81
 Db 65 VQAAIDYINGHQ 76

RESULT 7

US-10-089-019-34

; Sequence 34, Application US/10089019
 ; Patent No. 6951729
 ; GENERAL INFORMATION:
 ; APPLICANT: DEMOLFI, WALTER E. JR
 ; APPLICANT: KALLENBERG, HOWARD
 ; APPLICANT: LONSDALE, JOHN T.
 ; TITLE OF INVENTION: METHODS FOR MAKING AND USING FATTY ACID
 ; TITLE OF INVENTION: SYNTHESIS PATHWAY REAGENTS
 ; FILE REFERENCE: GM5068
 ; CURRENT APPLICATION NUMBER: US/10/089,019
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: PCT/US00/29451
 ; PRIOR FILING DATE: 2000-02-26
 ; PRIORITY NUMBER: 60/161,775
 ; PRIORITY FILING DATE: 1999-10-27
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 34
 ; LENGTH: 78
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli

Query Match 54.2%; Score 215; DB 2; length 78;
 Best Local Similarity 63.9%; Pred. No. 1.7e-18;
 Matches 46; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 10 ERVTKITIVDRIGVEDADVKLEASFKEFDLGASLDVVELVMELEDFDMEISDEDAEKIAT 69
 Db 6 ERVKKITGEOLGVQKQEVTNNASFVDLGASLDTVELVMALEEEFTEIPDEBAEKITT 65

Qy 70 VGDAVNYIQNQ 81
 Db 66 VQAAIDYINGHQ 77

RESULT 8

US-09-089-039A-7550

; Sequence 7550, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709-200001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A

Query Match 54.2%; Score 215; DB 2; Length 108;
 Best Local Similarity 63.9%; Pred. No. 2.7e-18;
 Matches 45; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 10 ERVTKITIVDRIGVEDADVKLEASFKEFDLGASLDVVELVMELEDFDMEISDEDAEKIAT 69
 Db 36 ERVKKITGEOLGVQKQEVTNNASFVDLGASLDTVELVMALEEEFTEIPDEBAEKITT 95

Qy 70 VGDAVNYIQNQ 81
 Db 96 VQAAIDYINGHQ 107

RESULT 9

US-09-252-991A-18645

; Sequence 18645, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 10716.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIORITY NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 18646
 ; LENGTH: 81
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa

Query Match 53.9%; Score 214; DB 2; Length 81;
 Best Local Similarity 59.0%; Pred. No. 2.4e-18;
 Matches 46; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Qy 4 GAQDTLERVTKITIVDRIGVEDADVKLEASFKEFDLGASLDVVELVMELEDFDMEISDEDAEKIAT 63
 Db 3 GMSTIEERVKVVAEQGVKEEBEVTNASFVDLGASLDTVELVMALEEEFTEIPDEB 62

Qy 64 AEKIATVGDAVNYIQNQ 81
 Db 63 AEKITVQEAIDYIVHQ 80

RESULT 10

US-09-252-991A-30132

; Sequence 30132, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: ASBURGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIORITY NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27

Query Match 54.2%; Score 215; DB 2; Length 108;
 Best Local Similarity 63.9%; Pred. No. 2.7e-18;
 Matches 45; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 10 ERVTKITIVDRIGVEDADVKLEASFKEFDLGASLDVVELVMELEDFDMEISDEDAEKIAT 69
 Db 36 ERVKKITGEOLGVQKQEVTNNASFVDLGASLDTVELVMALEEEFTEIPDEBAEKITT 95

Qy 70 VGDAVNYIQNQ 81
 Db 96 VQAAIDYINGHQ 107

RESULT 11

US-09-489-039A-7550

; Sequence 7550, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709-200001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A

Query Match 54.2%; Score 215; DB 2; Length 108;
 Best Local Similarity 63.9%; Pred. No. 2.7e-18;
 Matches 45; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 10 ERVTKITIVDRIGVEDADVKLEASFKEFDLGASLDVVELVMELEDFDMEISDEDAEKIAT 69
 Db 36 ERVKKITGEOLGVQKQEVTNNASFVDLGASLDTVELVMALEEEFTEIPDEBAEKITT 95

Qy 70 VGDAVNYIQNQ 81
 Db 96 VQAAIDYINGHQ 107

RESULT 12

US-09-252-991A-18646

; Sequence 18646, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 10716.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIORITY NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27

Query Match 53.9%; Score 214; DB 2; Length 81;
 Best Local Similarity 59.0%; Pred. No. 2.4e-18;
 Matches 46; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Qy 4 GAQDTLERVTKITIVDRIGVEDADVKLEASFKEFDLGASLDVVELVMELEDFDMEISDEDAEKIAT 63
 Db 3 GMSTIEERVKVVAEQGVKEEBEVTNASFVDLGASLDTVELVMALEEEFTEIPDEB 62

Qy 64 AEKIATVGDAVNYIQNQ 81
 Db 63 AEKITVQEAIDYIVHQ 80

RESULT 11
US-09-198-452A-308
; Sequence 308, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments, and treatment of infection
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198, 452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 308
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-308

Query Match Score 51.6%; Score 205; DB 2; Length 372;
Best Local Similarity 50.0%; Pred. No. 2.2e-16;
Matches 39; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 1 GRIGSAATLERTKILVDRGDEADVKLEASFKEIDGADSIDVWLMELDEDMEIS 60
Db 290 GPQCMDIETRVLVAFGEVECDIRLDSDFRNDFGAESLEVVWLMALAEARGVEIA 349

QY 61 DDAEAKTAVGDAVNQY 78
Db 350 DDDAERETVRQDIDY 367

RESULT 12
US-09-438-185A-297
; Sequence 297, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438, 185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108, 279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128, 606
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSEQ for Windows version 3.0
; SEQ ID NO 297

Query Match Score 51.6%; Score 205; DB 2; Length 372;
Best Local Similarity 50.0%; Pred. No. 2.2e-16;
Matches 39; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 1 GRIGSAATLERTKILVDRGDEADVKLEASFKEIDGADSIDVWLMELDEDMEIS 60
Db 290 GPQCMDIETRVLVAFGEVECDIRLDSDFRNDFGAESLEVVWLMALAEARGVEIA 349

QY 61 DDAEAKTAVGDAVNQY 78
Db 350 DDDAERETVRQDIDY 367

RESULT 13
US-09-328-352-4669
; Sequence 4669, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACTINETOBACTER BRAUmannI FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328, 352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4669
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-4669

Query Match Score 49.6%; Score 197; DB 2; Length 79;
Best Local Similarity 57.1%; Pred. No. 2.5e-16;
Matches 40; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 12 VTKIIVDRGDEADVKLEASFKEIDGADSIDVWLMELDEDMEISDEAKTAVG 71
Db 7 VIAIVEOLGVDPKEVNENSFIEDLNADSLTELINTLEEKFAFEISEDAEKURVG 66

QY 72 DAVNIVONQQ 81
Db 67 DVFTVIKKRQ 76

RESULT 14
US-09-107-532A-7143
; Sequence 7143, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 024354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US109/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998

ATTORNEY/AGENT INFORMATION:
 NAME: Azinillo, Pamela Deneke
 REGISTRATION NUMBER: 40 489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 893-5007
 TELEFAX: (781) 893-8277
 INFORMATION FOR SEQ ID NO: 7143:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 86 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1..86
 SEQUENCE DESCRIPTION: SEQ ID NO: 7143
 US-09-107-532A-7143

Query Match	45.3%	Score 180;	DB 2;	Length 86;
Best Local Similarity	50.7%	Pred. No. 3.	1e-14;	
Matches	37;	Conservative	13;	Missmatches 23; Indels 0;
				Gaps 0;

US-09-248-796A-1743B
; Sequence 17438, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMM
; TITLE OF INVENTION: FOR DIAGNOSTICS ANN
; FILE REFERENCE: 107196-132
; CURRENT APPLICATION NUMBER: US/09/248-7
; CURRENT FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17438
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-17438

Query Match 42.8%; **Score** 170; **DB 2;** **length** 111;
Best Local Similarity 40.0%; **Pred. No.** 6.9e-13; **Pred.**
Matches 32; **Conservative** 23; **Mismatches** 25; **Indels**

Qy 2 PLGSDATLERTVKILVDRLGWDEADVKLEASFKDIDGADSUDVWELVMELEDEFDNEISD 61
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
30 PISKDEVTSAIQLKTVAPLOESNITLESSFOKDGLDSLTDVTEALVALVEEFDLEIPD 89
Qy 62 EDAEKIATWGDAVNIVONQQ 81

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
 copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:41:34 ; Search time 118.075 Seconds
 (without alignments)
 483.997 Million cell updates/sec

Title: US-10-717-138-1

Perfect score: 397
 Sequence: 1 GPLGSAIDLERVTKIVDRL.....EDAEKIAITVGDAVNYIQNQQ 81

Scoring table: BL05IM62 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt 05.80:
 1: uniprot_sprot:
 2: uniprot_trembl:
 3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	370	93.2	77	1	ACP_BACSU	P80643	bacillus su
2	345	86.9	77	2	065JTO6_BACID	065jgf	bacillus li
3	315	79.3	77	2	0SLQ04_GROKA	0sl0q4	geobacillus
4	313	78.8	77	1	ACP_BACHD	0kka04	bacillus ha
5	311	78.3	77	1	ACP_BACSK	05wfm5	bacillus cl
6	302	76.1	77	1	ACP_BACAN	081wi1	bacillus an
7	302	76.1	77	1	ACP_BACCI	0732mm	bacillus ce
8	302	76.1	77	1	ACP_BACCR	081vv7	bacillus ce
9	302	76.1	77	1	ACP_BACZ	0536h6	bacillus ce
10	302	76.1	77	1	ACP_BACHX	08mbo3	bacillus ce
11	302	76.1	77	2	Q4MF03_BACCE	06mbo3	bacillus ce
12	284	71.5	77	1	ACP_LISIN	071y10	listeria mo
13	284	71.5	77	1	ACP_LISMF	053439	listeria mo
14	284	71.5	77	1	ACP_LISMO	088x06	oceanobacil
15	271	68.3	77	1	ACP_OCEIN	P43709	haemophilus
16	254	64.0	76	1	ACP_HAEIN	05rc88	mamnehimia
17	254	64.0	76	1	ACP_MANSW	Q9CJ83	haemophilus
18	254	64.0	76	1	Q4QF33_HABIE	Q9CJ85	pasteurella
19	62.7	62.7	76	1	ACP_PASMU	Q7pf6	symbiobacte
20	249	62.7	83	2	O67P06_SWYTH	Q4vk2	vibrio angu
21	247	62.2	77	2	Q4VK22_VIBAN	P02kw3	vibrio harv
22	244	61.5	76	1	ACP_VIBHA	P02kw2	vibrio par
23	244	61.5	76	1	ACP_VIBPA	Q5412	vibrio fisc
24	243	61.2	77	2	QSE412_VIBRI	Q9kq8	vibrio chol
25	60.2	77	1	ACP_VIBCH	Q8ep12	staphylococ	
26	59.9	77	1	ACP_STAEP	Q415t	staphylococ	
27	59.9	77	2	Q4L5T4_STAHJ	Q5mpv9	staphylococ	
28	59.9	77	2	Q5HPV9_STARQ	Q9fias	clostridium	
29	59.4	77	1	ACP_CLOBU	Q88g99	vibrio vuln	
30	59.4	77	1	ACP_VIBBU	Q7ml29	vibrio vuln	
31	59.4	78	1	ACP_VIBVY	Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,		

ALIGNMENTS

32	235	59.2	77	1	ACP_HAEDU	Q7wh6	haemophilus
33	234	58.9	77	1	ACP_STAM	P0a001	staphylococ
34	234	58.9	77	1	ACP_STRA	P0a002	staphylococ
35	234	58.9	77	1	ACP_STMAS	Q6g9y1	staphylococ
36	234	58.9	77	1	ACP_STMAS	P0a003	staphylococ
37	234	58.9	77	2	OSHKG0_STAAC	Q5hgk0	staphylococ
38	234	58.9	76	1	ACP_THTEN	Q8rg9w1	thermoanaer
39	233	58.7	78	2	Q7N3B7_PHOLI	Q7n3b7	phototrophabu
40	233	58.7	78	1	ACP_PHOPIR	Q9r6z3	photobacter
41	232	58.4	78	1	Q5QZ29_IDILO	Q5qz29	idiomarina
42	231	58.2	79	2	ACP_GROSIL	Q74cr8	leptospira
43	230	57.9	77	1	ACP_LIPIC	Q75Fw6	leptospira
44	230	57.9	77	1	ACP_LIPIN	Q8exx4	leptospira
45	230	57.9	77	1	ACP_LIEPIN		

Query Match 86.9%; Score 345; DB 2; Length 77;
 Best Local Similarity 93.4%; Pred. No. 8e-22; 3; Indels 0; Gaps 0;
 Matches 71; Conservative 2; Mismatches 3; Del 0; Insert 0;

RESULT 3
 Q5LQ4 GEOKA PRELIMINARY; PRT; 77 AA.
 ID Q5LQ4;
 AC 05LQ4;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)

DE Acyl carrier protein (ACP).
 ACBACD STANDARD; PRT; 77 AA.
 ID ACBACD
 AC Q9K404;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

Db 66 KIATVGDGVNMQ 81
 QY |||||||:::
 Db 62 KIATVGDGVNYSK 77

RESULT 4
 ACBACD STANDARD; PRT; 77 AA.
 ID ACBACD
 AC Q9K404;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

Db 66 KIATVGDGVNMQ 80
 QY |||||||:::
 Db 62 KIATVGDGVNYSK 76

RESULT 5
 ACBACSK STANDARD; PRT; 77 AA.
 ID ACBACSK
 AC Q9WFM5;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Acyl carrier protein (ACP).
 ACBACD STANDARD; PRT; 77 AA.
 ID ACBACD
 AC Q9K404;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

Db 66 KIATVGDGVNMQ 81
 QY |||||||:::
 Db 62 KIATVGDGVNYSK 77

DE Acyl carrier protein (ACP).
 AC Name=acpp; Synonyms=acpa; OrderedLocusNames=BH2490;
 OS *Bacillus halodurans*.
 OC *Bacillus halodurans*; *Bacillales*; *Bacillaceae*; *Bacillus*.
 NCBI_TaxID=86665;
 RN [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=C-125 / JCM 9153;
 RC MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuwara S.,
 RA Horikoshi K.;
 RA "Complete genome sequence of the alkaliophilic bacterium *Bacillus subtilis*".
 RT "Complete genome sequence of the alkaliophilic bacterium *Bacillus subtilis*".
 RL Nucleic Acids Res. 28:4317-4331(2000)
 CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid biosynthesis (By similarity).
 CC -!- PATHWAY: De novo fatty acid biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific serine of apo-ACP by acps. This modification is essential for activity because fatty acids are bound in thioester linkage to the sulphhydryl of the prosthetic group (By similarity).
 CC -!- SIMILARITY: Contains 1 acyl carrier domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC EMBL: BA00004; BAB#6209.1; -; Genomic_DNA.
 DR PIR; BB3961.
 DR HSSP; PB0643; IHX8.
 DR SNR; Q9KA04; 2-77.
 DR HMAP; MF_01217; -; 1.
 DR InterPro; IPR005081; ACP like.
 DR InterPro; IPR00231; Acyl carrier.
 DR InterPro; IPR006163; Phosphopanteth_bd.
 DR InterPro; IPR00162; Fpanne_S.
 DR Pfam; PF00550; pp-binding; 1.
 DR ProDom; PD000887; Acyl_carrier; 1.
 DR TIGRFAMS; TIGR00517; acyl_carrier; 1.
 DR PROSITE; PS50075; ACP DOMAIN; 1.
 DR PROSITE; PS00012; PHOSPHOPANTETHINE; 1.
 DR Complete proteome; Fatty acid biosynthesis; Lipid synthesis; KW Phosphopantetheine.
 FT BINDING 37 37 Phosphopantetheine (covalent) (By similarity).
 FT SEQUENCE 77 AA; 8558 MN; 3575CDPA45BA15CA CRC64;

Query Match 79.3%; Score 315; DB 2; Length 77;
 Best Local Similarity 81.6%; Pred. No. 4e-19; 6; Indels 0; Gaps 0;
 Matches 63; Conservative 8; Mismatches 4; Del 0; Insert 0;

QY 6 ADTLERVTKIVDRGVDERADVKLEASPFEDLGADSLDPUVMELEDFDMETSDDAE 65
 2 ADLVERVTKIVDRGVDERADVKLEASPFEDLGADSLDPUVMELEDFDMETSDDAE 61

Db 66 KIATVGDGVNMQ 80
 QY |||||||:::
 Db 62 KIATVGDGVNYSK 76

DT 13-SEP-2005 (T=EMBL; 31, Created)
 DT 13-SEP-2005 (T=EMBL; 31, last sequence update)
 DT 13-SEP-2005 (T=EMBL; 31, last annotation update)
 DE Acyl carrier protein.
 GN Name=acPP; ORFName=BCE_G9241_3833;
 OC *Bacillus cereus* G9241.
 OC *Bacteria*; *Firmicutes*; *Bacillales*; *Bacillaceae*; *Bacillus*;
 OC *Bacillus cereus* group.
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=G9241;
 RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
 RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
 RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
 RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Ger R.Z.,
 RA Rilstone J., Peterson S.N., Wayant R.S., Galloway D.R., Read T.D.,
 RA Popovic T., Fraser C.M.;
 RT "Identificatiⁿon of anthrax toxin genes in a *Bacillus cereus* associated
 with an illness resembling inhalation anthrax."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454 (2004).
 CC !- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAC01000080; BAL11450.1; -; Genomic DNA.
 SQ SEQUENCE 77 AA; 8513 MW; 8CCA3CBAE5DAA0B CRC64;

Query Match 76.1%; Score 302; DB 2; Length 77;
 Best Local Similarity 83.8%; Pred. No. 3 4e-18; Length 77;
 Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 6 ADTLERVKTIIVDRIGVDEAVKLEASPKEDLGADSLDVVELVMELEDFPMEISDAE 65
 DT 2 ADVLERTVKTIIVDRIGVTEEVPAASFKEIDLGADSLDVVELVMOLEDFPMEISDAE 61

OY 66 KIATVGDAVNYIQ 79
 Db 62 KIATVGDAVNTIES 75

RESULT 12

ACP_LISIN

ID ACP LISIN STANDARD; PRT; 77 AA.

AC P63440; Q9ZAK2; 28-FEB-2003 (Rel. 41, Created)
 DT 10-MAY-2005 (Rel. 41, Last sequence update)

DE Acyl carrier protein (ACP).
 GN Name=acPP; Synonyms=acPA; OrderedLocusNames=lin1920;
 OS *Listeria innocua*.
 OC *Bacteria*; *Firmicutes*; *Bacillales*; *Listeriaceae*; *Listeria*.
 RN [1] NCBI_TaxID=1642;

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CLIP 1162 / Serovar 6a;
 RX MEDLINE=21537279; PubMed=11679659; DOI=10.1126/science.1063447;
 RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Blecker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Darvuar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurgeot O.,
 RA Entian K.-D., Fischi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaeberst U., Kreft J., Kuhn M., Kunst F., Kurapati G.,
 RA Madueno E., Maitzmann A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordseik G., Novella S., de Pablos B., Perez-Blazquez J.-C., Purcell R.,
 RA Remml B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
 RT "Comparative genomics of *Listeria* species.";
 RL Science 294:849-852 (2001).
 CC !- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
 CC biosynthesis (By similarity).
 CC !- PATHWAY: De novo fatty acid biosynthesis.
 CC !- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC !- PTM: 4'-phosphopantetheine is transferred from CoA to a specific serine of apo-ACP by acPS. This modification is essential for activity because fatty acids are bound in thioester linkage to the biulidyl of the prosthetic group (By similarity).

CC !- SIMILARITY: Contains 1 acyl carrier domain.

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CC

CC DR EMBL; AL596170; CAC97150.1; -; Genomic_DNA.

CC DR PIR; AF1672; AF1672.

CC DR HSSP; 1HXB.

CC DR SMR; P63340; 2-74.

CC DR List-List; LIN01920; -.

CC DR HAMPRO; MF_01217; -; 1.

CC DR InterPro; IPR009081; ACP like.

CC DR InterPro; IPR003231; Acyl carrier.

CC DR InterPro; IPR006163; Phosphopanteth_bd.

CC DR InterPro; IPR006162; Peptidase_S.

CC DR Pfam; PF00550; PP-binding; 1.

CC DR PRODOM; PD000887; Acyl carrier; 1.

CC DR TIGRfams; TIGR00517; acyl_carrier; 1.

CC DR PROSITE; PS50075; ACP DOMAIN; 1.

CC DR PROSITE; PS50012; PHOSPHOPANTETHINE; 1.

CC KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis; Phosphopantetheine.

FT BINDING 37 37 Phosphopantetheine (covalent) (By similarity).

FT SO SEQUENCE 77 AA; 8335 MW; 8DE7E28C1F192E21 CRC64;

Query Match 71.5%; Score 284; DB 1; Length 77;
 Best Local Similarity 80.8%; Pred. No. 1.1e-16;
 Matches 59; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 6 ADTLERVKTIIVDRIGVDEAVKLEASPKEDLGADSLDVVELVMELEDFPMEISDAE 65
 DT 2 AEVLERVKTIIVDRIGVVEESKVTLAEASKEDLGADSLDVVELVMELEDFPMEISDAE 61

OY 66 KIATVGDAVNYIQ 78
 Db 62 NINTVSDAVKYIE 74

RESULT 13

ACP_LISMP

ID ACP LISMP STANDARD; PRT; 77 AA.

AC 071YLO; 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)

DE 10-MAY-2005 (Rel. 47, Last annotation update)

GN Name=acPP; OrderedLocusNames=LMOF2365_1834;
 OS *Listeria monocytogenes* (serotype 4b / strain F2365).
 OC *Bacteria*; *Firmicutes*; *Bacillales*; *Listeriaceae*; *Listeria*.
 RN [1] NCBI_TaxID=265669;

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15115801; DOI=10.1093/nar/gkh562;

RA Nelson K.E., Fouls D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
 RA Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
 RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beaman M.J.,
 RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
 RA Haft D.H., Selander R.K., Van Aken S.E., Khouri H.M., Fedorova N.,
 RA Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlrich G.A.,
 RA Bayles D.O., Luchansky J.B., Fraser C.M.,
 RT "Whole genome comparisons of serotype 4b and 1/2a strains of the foodborne pathogen *Listeria monocytogenes* reveal new insights into the core genome components of this species.";
 RT Nucleic Acids Res. 32:2396-2395 (2004).
 CC !- FUNCTION: Carrier of the growing fatty acid chain in fatty acid

CC biosynthesis (By similarity).
 CC --!- PATHWAY: De novo fatty acid biosynthesis.
 CC --!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC --!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
 CC series of apo-ACP by acPS. This modification is essential for
 CC activity because fatty acids are bound in thioester linkage to the
 CC sulphydryl of the prosthetic group (By similarity).
 CC --!- SIMILARITY: Contains 1 acyl carrier domain.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AE017328; AATW4604.1; -; Genomic_DNA.
 DR HSSP; P02201; IACP.
 DR SMR; Q71YH; 2-74.
 DR TIGR; IM02365; 1834; -.
 DR HAMAP; MF_01217; -; 1.
 DR InterPro; IPRO09081; ACP_like.
 DR InterPro; IPRO02331; Acyl_carrier.
 DR InterPro; IPRO06163; Phosphopanteth_bd.
 DR InterPro; IPRO06162; Peptidase_S.
 DR Pfam; PF00550; PP-binding; 1.
 DR ProDom; PD000887; Acyl_carrier; 1.
 DR TIGR00517; acyl_carrier; 1.
 DR PROSITE; PS50075; ACP_DOMAIN; 1.
 DR PROSITE; PS50012; PHOSPHOPANTETHINE; 1.
 DR KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Phosphopantetheine.
 FT BINDING 37 Phosphopantetheine (covalent) (BY similarity)
 FT SEQUENCE 77 AA; 8359 MW; 8DE7E28C1F192E21 CRC64;
 Query Match 71.5%; Score 284; DB 1; Length 77;
 Best Local Similarity 80.8%; Pred. No. 1.1e-16;
 Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 6 ADTLRVTKIVDRIGEADVKLEASPKEDIGADSIDVWLMELBDFDMEISDEAE 65
 DR 2 ARVLEYTKIVDRIGEASPKEDIGADSIDVWLMELBDFDMEISDEAE 61
 QY 66 KIATVGDAVVIQ 78
 Db 62 NINTVGDAVVIQ 74
 RESULT 14
 ACP_LISMO
 ID ACP_LISMO STANDARD; PRT; 77 AA.
 AC P6349; Q92AK2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl carrier protein (ACP).
 GN Name=acpp; OrderedLocusNames=lm01806;
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 NCBI_TAXID=1639;
 RN [1]
 RP NUCLEOTIDE_SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=2153729; PubMed=1679669; DOI=10.1126/science.1063447;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloch R., Brandt P., Chakraborty T.,
 RA Charbit A., Cheroni F., Couve E., de Darvvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussargent O.,
 RA Entian K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapati G.,
 RA Madueno E., Matson A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wahland J., Cosarart P.,
 RT "Comparative genomics of Listeria species.",
 RL Science 294:819-832 (2001).
 CC --!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
 CC biosynthesis (By similarity).
 CC --!- PATHWAY: De novo fatty acid biosynthesis.
 CC --!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC --!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
 CC serine of apo-ACP by acPS. This modification is essential for
 CC activity because fatty acids are bound in thioester linkage to the
 CC sulphydryl of the prosthetic group (By similarity).
 CC --!- SIMILARITY: Contains 1 acyl carrier domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AE017328; AATW4604.1; -; Genomic_DNA.
 DR HSSP; P02201; IACP.
 DR SMR; Q71YH; 2-74.
 DR TIGR; IM02365; 1834; -.
 DR HAMAP; MF_01217; -; 1.
 DR InterPro; IPRO09081; ACP_like.
 DR InterPro; IPRO02331; Acyl_carrier.
 DR InterPro; IPRO06163; Phosphopanteth_bd.
 DR InterPro; IPRO06162; Peptidase_S.
 DR Pfam; PF00550; PP-binding; 1.
 DR ProDom; PD000887; Acyl_carrier; 1.
 DR TIGR00517; acyl_carrier; 1.
 DR PROSITE; PS50075; ACP_DOMAIN; 1.
 DR PROSITE; PS50012; PHOSPHOPANTETHINE; 1.
 DR KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Phosphopantetheine.
 FT BINDING 37 Phosphopantetheine (covalent) (BY similarity)
 FT SEQUENCE 77 AA; 8359 MW; 8DE7E28C1F192E21 CRC64;
 Query Match 71.5%; Score 284; DB 1; Length 77;
 Best Local Similarity 80.8%; Pred. No. 1.1e-16;
 Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 6 ADTLRVTKIVDRIGEADVKLEASPKEDIGADSIDVWLMELBDFDMEISDEAE 65
 DR 2 ARVLEYTKIVDRIGEASPKEDIGADSIDVWLMELBDFDMEISDEAE 61
 QY 66 KIATVGDAVVIQ 78
 Db 62 NINTVGDAVVIQ 74
 RESULT 15
 ACP_OCEIH
 ID ACP_OCEIH STANDARD; PRT; 77 AA.
 AC Q8ERG6;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl carrier protein (ACP).
 GN Name=acpp; OrderedLocusNames=OB1525;
 OS Oceanobacillus_iheyensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus
 NCBI_TAXID=18210;
 RN [1]
 RP NUCLEOTIDE_SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=HTB831 / DSM 14371 / JCM 11309;
 RX MEDLINE=2220767; PubMed=1233576; DOI=10.1093/nar/gkf526;
 RA Takami H., Takaki Y., Uchiyama I.;
 RA "Genome sequence of Oceanobacillus iheyensis isolated from the Iheyama
 RT Ridge and its unexpected adaptive capabilities to extreme

RT environments.";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
 CC biosynthesis (By similarity).
 CC -!- PATHWAY: De novo fatty acid biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
 CC serine of apo-ACP by acPS. This modification is essential for
 CC activity because fatty acids are bound in thioester linkage to the
 CC sulfhydryl of the prosthetic group (By similarity).
 CC -!- SIMILARITY: Contains 1 acyl carrier domain.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; BA000028; BAC13481.1; -; Genomic_DNA.
 DR HSSP; P80643; IF80.
 DR SMR; QBER06; 2-76.
 DR HAMAP; ME_01217; -; 1.
 DR InterPro; IPR000881; ACP like.
 DR InterPro; IPR003231; Acyl carrier.
 DR InterPro; IPR006163; Phosphopanteth_bd.
 DR InterPro; IPR005162; Fpancre_S.
 DR Pfam; PF00550; PP-binding; 1.
 DR ProDom; PDO00887; Acyl_carrier; 1.
 DR TIGRFAMS; TIGR00517; acyl_carrier; 1.
 DR PROSITE; PS50075; ACP DOMAIN; 1.
 DR PROSITE; PS00012; PHOSPHOPANTETHINE; FALSE NEG.
 DR KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Phosphopantetheine.
 FT BINDING 37 phosphopantetheine (covalent) (By
 FT SQ SEQUENCE 77 AA; 87/32 MW: E78F70BB5F7D4C77 CRC64;
 Query Match 68.3%; Score 271; DB 1; Length 77;
 Best Local Similarity 72.0%; Pred. No. 1.4e-15;
 Matches 54; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
 Ov 6 ADPLMLERVKTVIIRGLVEDADVKLEASFKEDIDGADSIDDVVEVWMELEDFPOMEISDAE 65
 Db 2 AEVFDRVKELIIDRLDVBEESKTMASFKDDADSDIDVNEVWMELEDFPOMEIAEDAE 61
 Ov 66 KIAATVGDAVNLYQNO 80
 Db 62 KINNVGDAVDYINSK 76

Search completed: December 21, 2005, 13:54:38
 Job time : 119.075 secs

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OM protein - protein search, using sw model									
Title:	US-10-717-138-1								
Perfect score:	397								
Sequence:	1 GPGSGADTLERTVTKIVRL.....EDERKLTAVGDAVNLYNQQ 81								
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5								
Searched:	283416 seqs, 96216763 residues								
Total number of hits satisfying chosen parameters:	283416								
Minimum DB seq length:	0								
Maximum DB seq length:	200000000								
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries								
Database :	PIR 80:*								
	1: pir1:*								
	2: pir2:*								
	3: pir3:*								
	4: pir4:*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match	Length	DB	ID	Description			
							JC4822	acetyl carrier protein - <i>Bacillus subtilis</i>	RESULTS 1
1	370	93.2	77	2	JC4822	N;Alternate names: 8.5K protein C;Species: <i>Bacillus subtilis</i> C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004 C;Accession: JC4822; A695822 R;Oguro, A.; Kakeshita, H.; Takamatsu, H.; Nakamura, K.; Yamane, K. Gene 172, 17-21, 1996 A;Title: The effect of Srb, a homologue of the mammalian SRP receptor alpha-subunit, on A;Reference number: JC4819; MUID:9625747; PMID:8654983 A;Molecule type: DNA A;Cross-references: UNIPARC:UP100000603BF; DDBJ:D64116; NID:91389548; PIR:R;Kunst, F.; Ogasawara, N.; Moeser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteletti, C.; Bruni, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, C.; Capuano, V.; Carter, N.M.; Choi A.; Enrich, S.D.; Ellmer, S.P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997 A;Authors: Fouleg, C.R.; Henaut, A.; Hilbert, H.; Holsapple, S.; Hullio, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lardinois, A.; Lardinois, S.; Maudel, Y.; Authors: Lauber, J.; Lazarovic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maudel, Y.; Ogawa, K.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Satoh, T.; Scanlon, A.; Authors: Schilke, S.; Schofne, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, A.; keuchli, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zunstein, E.; Yoshikawa, H.; Danchin, A. A;Cross-references: UniProt:Q9WZD1; UniProt:Q9WZD2; UniProt:Q9WZD3; UniProt:Q9WZD4; UniProt:Q9WZD5; UniProt:Q9WZD6; UniProt:Q9WZD7; UniProt:Q9WZD8; UniProt:Q9WZD9; UniProt:Q9WZD10; UniProt:Q9WZD11; UniProt:Q9WZD12; UniProt:Q9WZD13; UniProt:Q9WZD14; UniProt:Q9WZD15; UniProt:Q9WZD16; UniProt:Q9WZD17; UniProt:Q9WZD18; UniProt:Q9WZD19; UniProt:Q9WZD20; UniProt:Q9WZD21; UniProt:Q9WZD22; UniProt:Q9WZD23; UniProt:Q9WZD24; UniProt:Q9WZD25; UniProt:Q9WZD26; UniProt:Q9WZD27; UniProt:Q9WZD28; UniProt:Q9WZD29; UniProt:Q9WZD30; UniProt:Q9WZD31; UniProt:Q9WZD32; UniProt:Q9WZD33; UniProt:Q9WZD34; UniProt:Q9WZD35; UniProt:Q9WZD36; UniProt:Q9WZD37; UniProt:Q9WZD38; UniProt:Q9WZD39; UniProt:Q9WZD40; UniProt:Q9WZD41; UniProt:Q9WZD42; UniProt:Q9WZD43; UniProt:Q9WZD44; UniProt:Q9WZD45; UniProt:Q9WZD46; UniProt:Q9WZD47; UniProt:Q9WZD48; UniProt:Q9WZD49; UniProt:Q9WZD50; UniProt:Q9WZD51; UniProt:Q9WZD52; UniProt:Q9WZD53; UniProt:Q9WZD54; UniProt:Q9WZD55; UniProt:Q9WZD56; UniProt:Q9WZD57; UniProt:Q9WZD58; UniProt:Q9WZD59; 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UniProt:Q9WZD566; UniProt:Q9WZD567; UniProt:Q9WZD568; UniProt:Q9WZD569; UniProt:Q9WZD570; UniProt:Q9WZD571; UniProt:Q9WZD572; UniProt:Q9WZD573; UniProt:Q9WZD574; UniProt:Q9WZD575; UniProt:Q9WZD576; UniProt:Q9WZD577; UniProt:Q9WZD578; UniProt:Q9WZD579; UniProt:Q9WZD580; UniProt:Q9WZD581; UniProt:Q9WZD582; UniProt:Q9WZD583; UniProt:Q9WZD584; UniProt:Q9WZD585; UniProt:Q9WZD586; UniProt:Q9WZD587; UniProt:Q9WZD588; UniProt:Q9WZD589; UniProt:Q9WZD590; UniProt:Q9WZD591; UniProt:Q9WZD592; UniProt:Q9WZD593; UniProt:Q9WZD594; UniProt:Q9WZD595; UniProt:Q9WZD596; UniProt:Q9WZD597; UniProt:Q9WZD598; UniProt:Q9WZD599; UniProt:Q9WZD600; UniProt:Q9WZD601; UniProt:Q9WZD602; UniProt:Q9WZD603; UniProt:Q9WZD604; UniProt:Q9WZD605; UniProt:Q9WZD606; UniProt:Q9WZD607; UniProt:Q9WZD608; UniProt:Q9WZD609; UniProt:Q9WZD610; UniProt:Q9WZD611; UniProt:Q9WZD612; UniProt:Q9WZD613; UniProt:Q9WZD614; UniProt:Q9WZD615; UniProt:Q9WZD616; UniProt:Q9WZD617; UniProt:Q9WZD618; UniProt:Q9WZD619; UniProt:Q9WZD620; UniProt:Q9WZD621; UniProt:Q9WZD622; UniProt:Q9WZD623; UniProt:Q9WZD624; UniProt:Q9WZD625; UniProt:Q9WZD626; UniProt:Q9WZD627; UniProt:Q9WZD628; UniProt:Q9WZD629; UniProt:Q9WZD630; UniProt:Q9WZD631; UniProt:Q9WZD632; UniProt:Q9WZD633; UniProt:Q9WZD634; UniProt:Q9WZD635; UniProt:Q9WZD636; UniProt:Q9WZD637; UniProt:Q9WZD638; UniProt:Q9WZD639; UniProt:Q9WZD640; UniProt:Q9WZD641; UniProt:Q9WZD642; UniProt:Q9WZD643; UniProt:Q9WZD644; UniProt:Q9WZD645; UniProt:Q9WZD646; UniProt:Q9WZD647; UniProt:Q9WZD648; UniProt:Q9WZD649; UniProt:Q9WZD650; UniProt:Q9WZD651; UniProt:Q9WZD652; UniProt:Q9WZD653; UniProt:Q9WZD654; UniProt:Q9WZD655; UniProt:Q9WZD656; UniProt:Q9WZD657; UniProt:Q9WZD658; UniProt:Q9WZD659; UniProt:Q9WZD660; UniProt:Q9WZD661; UniProt:Q9WZD662; UniProt:Q9WZD663; UniProt:Q9WZD664; UniProt:Q9WZD665; UniProt:Q9WZD666; UniProt:Q9WZD667; UniProt:Q9WZD668; UniProt:Q9WZD669; UniProt:Q9WZD670; UniProt:Q9WZD671; UniProt:Q9WZD672; UniProt:Q9WZD673; UniProt:Q9WZD674; UniProt:Q9WZD675; UniProt:Q9WZD676; UniProt:Q9WZD677; 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UniProt:Q9WZD790; UniProt:Q9WZD791;			

Db	2 ADTLETRVTKIVDRIGVDEADVKLEASFEDLQDSIDVVEDVMEJEDFMEISDDDAE 61	Db	2 AAVLEKVTIKIVDRIGVDEADVKLEASFEDLQDSIDVVEDVMEJEDFMEISDDDAE 61
Qy	66 KIATVGDAVNVIQ 81	Qy	66 KIATVGDAVNVIQ 78
Db	62 KIATVGDAVNVIQ 77	Db	62 NINTVGDAVKE 74
		RESULT 4	
		AF1672	acyl carrier protein homolog acpa [imported] - listeria innocua (strain Clip11262)
		C;Species: Listeria innocua	C;Species: Listeria innocua (strain Clip11262)
		C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
		C;Accession: AF1672	C;Accession: AF1672
		R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Bagner, F.; Berche, P.; Blecker, D.; Jones, L.M.; Karst, U.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Duburgot, O.; Entian, K.D.; Fsihi, H.; Science 294, 849-852, 2001.	R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Bagner, F.; Berche, P.; Blecker, D.; Jones, L.M.; Karst, U.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Duburgot, O.; Entian, K.D.; Fsihi, H.; Science 294, 849-852, 2001.
		D.; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madero, E.; Maitouram, A.; Mattok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Reference number: AB1077; PMID:21537279; PMID:1679669	D.; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madero, E.; Maitouram, A.; Mattok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Reference number: AB1077; PMID:21537279; PMID:1679669
		A;Cross-references: UNIPROT:Q9KA04; UNIPARC:UPI0000125360; GB:AP001515; GB:BA000004; NID:1679669	A;Cross-references: UNIPROT:Q9KA04; UNIPARC:UPI0000125360; GB:AP001515; GB:BA000004; NID:1679669
		A;Experimental source: strain C-125	A;Experimental source: strain C-125
		C;Genetics:	C;Genetics:
		A;Gene: acpa	A;Gene: acpa
		C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology	C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
		C;Keywords: carrier protein	C;Keywords: carrier protein
		RESULT 3	
		AF1300	acyl carrier proteins homolog acpa [imported] - Listeria monocytogenes (strain EGD-e)
		C;Species: Listeria monocytogenes	C;Species: Listeria monocytogenes (strain EGD-e)
		C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
		C;Accession: AF1300	C;Accession: AF1300
		R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Domínguez-Bernal, G.; Buchaud, E.; Durand, L.; Dusburgé, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001.	R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Domínguez-Bernal, G.; Buchaud, E.; Durand, L.; Dusburgé, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001.
		D.; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madero, E.; Maitouram, A.; Mattok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species. A;Reference number: AB1077; PMID:21537279; PMID:1679669	D.; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madero, E.; Maitouram, A.; Mattok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species. A;Reference number: AB1077; PMID:21537279; PMID:1679669
		A;Experimental source: strain C-125	A;Experimental source: strain C-125
		A;Status: preliminary	A;Status: preliminary
		A;Molecule type: DNA	A;Molecule type: DNA
		A;Residues: 1-77 <GLA>	A;Residues: 1-77 <GLA>
		A;Cross-references: UNIPROT:Q92AK2; UNIPARC:UPI0000555AC; GB:NC_003210; PIDN:CA99894.1	A;Cross-references: UNIPROT:Q92AK2; UNIPARC:UPI0000555AC; GB:NC_003210; PIDN:CA99894.1
		A;Experimental source: strain EGD-e	A;Experimental source: strain EGD-e
		C;Genetics:	C;Genetics:
		A;Gene: acpa	A;Gene: acpa
		C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology	C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
		C;Keywords: carrier protein	C;Keywords: carrier protein
		RESULT 5	
		C64051	acyl carrier protein - Haemophilus influenzae (strain Rd KW20)
		C;Species: Haemophilus influenzae	C;Species: Haemophilus influenzae (strain Rd KW20)
		C;Accession: C64051	C;Accession: C64051
		R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Goeyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weilman, J.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995.	R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Goeyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weilman, J.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995.
		D.; Authors: Gnehn, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A.; Reference number: A64000; PMID:95350650; PMID:7542800	D.; Authors: Gnehn, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A.; Reference number: A64000; PMID:95350650; PMID:7542800
		A;Accession: C64051	A;Accession: C64051
		A;Status: nucleic acid sequence not shown; translation not shown	A;Status: nucleic acid sequence not shown; translation not shown
		A;Molecule type: DNA	A;Molecule type: DNA
		A;Residues: 1-76 <TIGR>	A;Residues: 1-76 <TIGR>
		A;Cross-references: UNIPROT:P43709; UNIPARC:UPI0000125370; GB:U32701; GB:L42023; NID:932	A;Cross-references: UNIPROT:P43709; UNIPARC:UPI0000125370; GB:U32701; GB:L42023; NID:932
		C;Genetics:	C;Genetics:
		A;Gene: acpa	A;Gene: acpa
		C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology	C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
		C;Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; phosphoprotein	C;Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; phosphoprotein
		F1-72/Domain: acyl carrier protein homology <ACP>	F1-72/Domain: acyl carrier protein homology <ACP>
		F35/Binding site: phosphopantetheine (Ser) (covalent) #status predicted	F35/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 64.0%; Score 254; DB 2; Length 76;
 Best Local Similarity 72.2%; Pred. No. 6.6e-16; Indels 0; Gaps 0;
 Matches 52; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 10 ERVTKIVDRIGVDEADVKLFAASFKEKGASDLSDVWLMLEDEDEMEISDEDAEKIAT 69
 Db 5 ERVKKIVVEQGVKEEDVKPASFVEDLGASDLSDVWLMLEDEDEMEISDEDAEKIAT 64

RESULT 6

T12052 acyl carrier protein - *Vibrio harveyi*
 C;Species: *Vibrio harveyi*
 C;Description: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T12052
 R;Shen, Z.; Byers, D.M.
 J; Bacteriol. 178, 571-573, 1996
 A;Title: Isolation of *Vibrio harveyi* acyl carrier protein and the fabG, acpp and fabr genes
 A;Reference number: 217395; MUID:96134997; PMID:8550484

A;Accession: T12052
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-77 <SHE>
 A;Cross-references: UNIPROT:P55337; UNIPARC:UPI0000009F93; EMBL:U39441; NID:gi173839; PI

A;Experimental source: strain B392
 C;Genetics:
 A;Gene: acpp
 C;Function:
 A;Description: carrier of the growing fatty acid chain; growing fatty acid chain is covalently attached to the acyl carrier protein
 A;Pathway: fatty acid biosynthesis
 C;Superfamily: acyl-peptidyl carrier protein; acyl carrier protein homology
 C;Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; phosphoprotein
 P;37/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 61.5%; Score 244; DB 2; Length 77;
 Best Local Similarity 69.4%; Pred. No. 5.1e-15; Mismatches 50; Conservative 10; Indels 0; Gaps 0;
 Matches 50; Mismatches 12; Indels 0; Gaps 0;

Qy 10 ERVIKITVDRIGVDEADVKLFAASFKEKGASDLSDVWLMLEDEDEMEISDEDAEKIAT 69
 Db 6 ERVKKIVVEQGVKEEDVKPASFVEDLGASDLSDVWLMLEDEDEMEISDEDAEKIAT 65

Qy 70 VGDAVNYIQNQQ 81
 Db 66 VQAADIVYNSAQ 77

RESULT 7

E82128 acyl carrier protein VC2020 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
 C;Species: *Vibrio cholerae*
 C;Accession: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 28-Jul-2003

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Fritchman, D.; Brinkac, M.D.; VanAken, J.; Basa, S.; Qin, H.; Dragoi, I.; Seligson, F.; Richardson, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: E82128
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-110 <HEI>
 A;Cross-references: UNIPARC:UPI000164B85; GB:AE004276; GB:AE003852; PID:9656555; PI

A;Experimental source: serogroup O1; Strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC2020
 A;Map position: 1

RESULT 8

F97115 acyl carrier protein, ACP [imported] - *Clostridium acetobutylicum*
 C;Species: *Clostridium acetobutylicum*
 C;Accession: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J; Bacteriol. 183, 4823-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*
 A;Reference number: A96900; MUID:21359325; PMID:121359325

A;Accession: F97115
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-77 <KUR>
 A;Cross-references: UNIPROT:Q971A5; UNIPARC:UPI000125356; GB:AE001437; PID:AAK79713.1;
 A;Experimental source: *Clostridium acetobutylicum* ATCC824
 C;Genetics:
 A;Gene: CAD1747
 C;Superfamily: acyl-peptidyl carrier protein; acyl carrier protein homology
 C;Keywords: carrier protein

Query Match 59.4%; Score 236; DB 2; Length 77;
 Best Local Similarity 60.9%; Pred. No. 2.6e-14; Mismatches 42; Conservative 18; Indels 0; Gaps 0;
 Matches 42; Mismatches 18; Indels 0; Gaps 0;

Qy 10 ERVIKITVDRIGVDEADVKLFAASFKEKGASDLSDVWLMLEDEDEMEISDEDAEKIAT 69
 Db 4 ERVKKIVVEQGVKEEDVKPASFVEDLGASDLSDVWLMLEDEDEMEISDEDAEKIAT 63

Qy 70 VGDAVNYIQ 78
 Db 64 VGDAVNYIK 72

RESULT 9

E82128 acyl carrier protein [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
 C;Species: *Vibrio cholerae*
 C;Accession: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 28-Jul-2003

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Inoue, R.; Kaito, C.; Sekimizu, K.; Oguma, A.; Mizutani-Uti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Oguma, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
 A;Reference number: A89758; MUID:21311952; PMID:1418146

A;Accession: C89896
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-77 <KUR>
 A;Cross-references: UNIPROT:Q99QNT; UNIPARC:UPI000125385; GB:BA000018; PID:gi13701032; PI

A;Experimental source: strain N315
 C;Genetics:
 A;Gene: hmrB
 A;Map position: 1

C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
 C;Keywords: carrier protein

Query Match 58.9%; Score 234; DB 2; Length 77;
 Best Local Similarity 65.8%; Pred. No. 3_9e-14; Mismatches 16; Indels 0; Gaps 0;

Matches 48; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 7 DPLERVKIVLVRIGVDAVDKVLKEASFKEDGADSILDVVELMELDEFDMEISDEAK 66
 Db 2 ENFDKVQDILVDRIGVDAVDKVTEDASPKDDLGADSILDVVELMELDEFDGEIPDEAEK 61

Qy 67 IATVGDAVINYI 79
 Db 62 INTVFGDAVKFINS 74

RESULT 10

AC0195
 acyl carrier protein [imported] - *Yersinia pestis* (strain C992)
 C;Species: *Yersinia pestis*
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AC0195
 R;Parthill, J. ; Wren, B.W. ; Thomson, N.R. ; Tibball, R.W. ; Holden, M.T.G. ; Prentice, M.B. ; Deno-Tarara, A.M. ; Chillingworth, T. ; Cronin, A. ; Davies, R.M. ; Dongan, G. ; Ill, M. ; Rutherford, K. ; Simmonds, M. ; Skelton, J. ; Stevens, K. ; Whitehead, S. ; Barrell, B. ; Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AC0195
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-78 <KUR>
 A;Cross-references: UNIPROT:Q8ZFT4; UNIPARC:UPI000165B20; GB:AL590842; PIDN:CAC90422.1; C;Genetics:

Query Match 57.1%; Score 226.5; DB 2; Length 78;
 Best Local Similarity 68.5%; Pred. No. 1_8e-13; Mismatches 8; Indels 1; Gaps 1;

Matches 50; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

Qy 10 ERVTKIVLVRIGVDAVDKVLKEASFKEDGADSILDVVELMELDEFDMEISDEAKIAT 69
 Db 6 ERYKKIVIEQGLYKEDEVKVASFVDLGADSLTVELVMALEEEFDTIEPDEAEKITT 65

Qy 70 VGDAVNYIQ-NQQ 81
 Db 66 VQAIDFINANQQ 78

RESULT 11

A70448
 acyl carrier protein - *Aquifex aeolicus*
 C;Species: *Aquifex aeolicus*
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
 C;Accession: A70448
 R;Deckert, G. ; Warren, P.V. ; Gaasterland, T. ; Young, W.G. ; Lenox, A.L. ; Graham, D.E. ; On Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
 A;Reference number: A70300; MUID:98196666; PMID:9537320
 A;Accession: A70448
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-78 <AQF>
 A;Cross-references: UNIPROT:O67611; UNIPARC:UPI0000566C2; GB:AE000752; NID:92984021; PI
 A;Experimental source: strain VF5
 C;Genetics:
 A;Gene: acpp
 C;Function:

A;Description: carrier of the growing fatty acid chain; growing fatty acid chain is covalently attached to the protein

RESULT 12

T44335
 acyl carrier protein [imported] - *Moritella marina*
 C;Species: *Moritella marina*
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T44335
 R;Morita, N. ; Ueno, A. ; Tanaka, M. ; Ogiya, S. ; Hoshino, T. ; Kawasaki, K. ; Yumoto, I. ; Ito, Biotechnol. Lett. 21, 641-646, 1999
 A;Title: Cloning and sequencing of clustered genes involved in fatty acid biosynthesis f. A;Reference number: 222768
 A;Accession: T44335
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-78 <MR>
 A;Cross-references: UNIPROT:Q9RA22; UNIPARC:UPI00016EOF2; EMBL:AB021978; PIDN:BA85257.1; C;Genetics:
 A;Experimental source: ATCC 15381
 A;Note: acPP
 C;Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
 F;37/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 55.4%; Score 220; DB 2; Length 78;
 Best Local Similarity 64.7%; Pred. No. 6.7e-13; Mismatches 12; Indels 0; Gaps 0;

Matches 44; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 10 ERVTKIVLVRIGVDAVDKVLKEASFKEDGADSILDVVELMELDEFDMEISDEAKIAT 69
 Db 6 ERYKKIVIEQGLYKEDEVKVASFVDLGADSLTVELVMALEEEFDTIEPDEAEKITT 65

Qy 70 VGDAVNYI 77
 Db 66 VQAIDYV 73

RESULT 13

AG2223
 acyl carrier protein [imported] - *Nostoc* sp. (strain PCC 7120)
 C;Species: *Nostoc* sp. PCC 7120
 C;Accession: AG2223
 A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C;Accession: AG2223
 R;Kaneko, T. ; Nakamura, Y. ; Wolk, C.P. ; Kuritz, T. ; Sasamoto, S. ; Watanabe, A. ; Iriuchi, T. ; Nakazaki, N. ; Shimpo, S. ; Sugimoto, M. ; Takazawa, M. ; Yamada, M. ; Yasuda, M. ; Tabata, S. ; DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
 A;Reference number: AB1607; MUID:21595285; PMID:11759840
 A;Accession: AG2223
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-84 <KUR>
 A;Cross-references: UNIPROT:P58553; UNIPARC:UPI0001655CF; GB:BA000019; PIDN:BA875041.1; C;Experimental source: strain PCC 7120

Thu Dec 22 11:00:01 2005

us-10-717-138-1.rpr

Page 6

Search completed: December 21, 2005, 13:49:38
Job time : 10.4776 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:40:03 ; Search time 107.194 Seconds
(without alignments)
332.012 Million cell updates/sec

Title: US-10-717-138-1
Perfect score: 397
Sequence: 1 GPLGSAQTLERVVIKVIVDRL... EDAEKIATVGDAVNYIQNQQ 81

Scoring table: BLOSUM62
GapOp 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqP1980s:*
- 2: geneseqP1990s:*
- 3: geneseqP2000s:*
- 4: geneseqP2001s:*
- 5: geneseqP2002s:*
- 6: geneseqP2003as:*
- 7: geneseqP2003bs:*
- 8: geneseqP2004as:*
- 9: geneseqP2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	397	100.0	81	5 AAU10693
2	307	77.3	80	6 ABU18284
3	284	71.5	77	5 ABBA9632
4	284	71.5	77	6 ABU32958
5	254	64.0	76	4 ABU35380
6	254	64.0	76	6 ABU3165
7	249	62.7	76	6 ABU39519
8	239	60.2	110	6 ABU39494
9	238	59.9	77	6 ABU3867
10	238	59.9	77	6 ABU2995
11	238	59.9	79	5 ABP39964
12	238	59.9	79	8 ADPS03306
13	236	59.4	77	6 ABU23599
14	234	58.9	77	4 AAU37508
15	234	58.9	77	4 AAU37209
16	234	58.9	77	4 AAE02204
17	234	58.9	77	6 ABP02204
18	234	58.9	77	6 ABM7195
19	234	58.9	77	9 ADW94686
20	232	58.4	73	4 AAU33966
21	232	58.4	77	4 AAU36531
22	227	57.2	79	6 ABU23521
23	57.1	78	6 ABP0649	
24	56.7	78	6 ADP07671	

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

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15	234	58.9	77	4 AAU37209
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18	234	58.9	77	6 ABM7195
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

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- 6: geneseqP2003as:*
- 7: geneseqP2003bs:*
- 8: geneseqP2004as:*
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14	234	58.9	77	4 AAU37508
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16	234	58.9	77	4 AAE02204
17	234	58.9	77	6 ABP02204
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23	57.1	78	6 ABP0649	
24	56.7	78	6 ADP07671	

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqP1980s:*
- 2: geneseqP1990s:*
- 3: geneseqP2000s:*
- 4: geneseqP2001s:*
- 5: geneseqP2002s:*
- 6: geneseqP2003as:*
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- 8: geneseqP2004as:*
- 9: geneseqP2005s:*

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24	56.7	78	6 ADP07671	

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqP1980s:*
- 2: geneseqP1990s:*
- 3: geneseqP2000s:*
- 4: geneseqP2001s:*
- 5: geneseqP2002s:*
- 6: geneseqP2003as:*
- 7: geneseqP2003bs:*
- 8: geneseqP2004as:*
- 9: geneseqP2005s:*

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9	238	59.9	77	6 ABU3867
10	238	59.9	77	6 ABU2995
11	238	59.9	79	5 ABP39964
12	238			

CC represents *B. subtilis* ACP used to grow ACP/ACPS complex crystals
 XX Sequence 81 AA;
 SQ

Query Match 100.0%; Score 397; DB 5; Length 81;
 Best Local Similarity 100.0%; Pred. No. 1.8e-36; Mismatches 0; Indels 0; Gaps 0;
 Matches 81; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 GPGLGSDTLERTRKILIVDRIGDEADVYKLEASFKEKGADSLDVVLMELDEFMEIS 60
 Db 1 GPLGSADTLERTRKILIVDRIGDEADVYKLEASFKEKGADSLDVVLMELDEFMEIS 60

Qy 61 DDEDAEKIATVGDAVNQIQQ 81
 Db 61 DDEDAEKIATVGDAVNQIQQ 81

RESULT 2

ABU18284 standard; protein; 80 AA.
 ID ABU18284;
 AC ABU18284;
 XX DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #3811.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS Bacillus anthracis.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PP 21-MAR-2002; 2002WO-US009107.
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342933P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.

(ELITR-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 DR WPI; 2003-029926/02.
 XX N-PSDB; ACa22154.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 25; SBQ ID NO 46208; 1766pp; English.

PS The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an

RESULT 3

ABB49632 standard; protein; 77 AA.
 ID ABB49632;
 XX AC ABB49632;
 XX DT 05-FEB-2002 (first entry)
 XX DE Listeria monocytogenes protein #2336.
 XX KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.
 OS Listeria monocytogenes.
 XX PN WO200177335-A2.
 XX PD 18-OCT-2001.
 XX PP 11-APR-2001; 2001WO-FR001118.
 XX PR 11-APR-2000; 2000FR-00004629.
 XX PA (INSP) INST PASTEUR.

XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
 PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-Garcia P, Tellez-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Madueno E, De Pablos B, Weiland J, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;
 XX DR WPI; 2002-010914/01.

XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 PT and prevention of Listeria and related bacterial infections, and related
 PT polypeptides.
 XX PS Claim 6; SEQ ID NO 2337; 192pp; French.

CC
CC The present invention relates to the genome sequence of *Listeria*
CC moncytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in *L.*
CC moncytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of *L.* moncytogenes and related organisms, and
CC biosynthesis and biodegradation, especially biosynthesis of Vitamin
B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate *L.* moncytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by *L.*
CC moncytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 77 AA;

Query Match 71.5%; Score 284; DB 5; Length 77;
Best Local Similarity 80.8%; Pred. No. 6.6e-24;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 6 ADTLERVKIIVDRIGEADVKLEASFKEDIGADSIDVVELVMELEDEFDMEISDBAE 65
Db 2 AEVLEKVKIIVDRIGEESKVLEASFKEIDGADSIDVVELVMELEDEFGEVEISGDAE 61
QY 66 KIATVGDAVNYIQ 78
Db 62 NINTVGDAVKYE 74

XX Sequence 77 AA;

RESULT 4
ABU32958
ID ABU32958 standard; protein; 77 AA.
XX
AC ABU32958;
DT 19-JUN-2003 (first entry)
DE Protein encoded by Prokaryotic essential gene #18485.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Listeria monocytogenes.
XX
PN WO200277183-A2.

Query Match 71.5%; Score 284; DB 5; Length 77;
Best Local Similarity 80.8%; Pred. No. 6.6e-24;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 6 ADTLERVKIIVDRIGEADVKLEASFKEDIGADSIDVVELVMELEDEFDMEISDBAE 65
Db 2 AEVLEKVKIIVDRIGEESKVLEASFKEIDGADSIDVVELVMELEDEFGEVEISGDAE 61
QY 66 KIATVGDAVNYIQ 78
Db 62 NINTVGDAVKYE 74

XX Sequence 77 AA;

RESULT 5
AAU35380
ID AAU35380 standard; protein; 76 AA.
XX
AC AAU35380;
XX
DT 14-FEB-2002 (first entry)
DE *Haemophilus influenzae* cellular proliferation protein #21.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
OS *Haemophilus influenzae*.
PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Travick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
PR 06-SEP-2001; 2001US-009193.
PR 25-OCT-2001; 2001US-0342923P.
PR 05-FEB-2002; 2002US-0072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
(ELIT-) ELITRA PHARM INC.
XX
PA WPI; 2003-02926/02.
DR N-PSDB; ACA36828.

XX Sequence 77 AA;

Query Match 71.5%; Score 284; DB 6; Length 77;
Best Local Similarity 80.8%; Pred. No. 6.6e-24;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 6 ADTLERVKIIVDRIGEADVKLEASFKEDIGADSIDVVELVMELEDEFDMEISDBAE 65
Db 2 AEVLEKVKIIVDRIGEESKVLEASFKEIDGADSIDVVELVMELEDEFGEVEISGDAE 61
QY 66 KIATVGDAVNYIQ 78
Db 62 NINTVGDAVKYE 74

XX Sequence 77 AA;

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
K. pneumoniae or *P. aeruginosa*. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp://wipo.int/pub/published_pct_sequences

PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-025731P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 XX PI Yamamoto RT, Xu HH;
 XX DR WPI; 2001-611495/70.
 DR N-PSDB; AAS53239.

XX PT New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.

PS Example 3; SEQ ID NO 10973; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 76 AA:

Query Match	64.0%	Score	254;	DB	4;	Length	76;
Best Local Similarity	72.2%	Pred.	No.	1.4e-20;	Mismatches	52;	Conservative
Matches	8;	Mismatches	12;	Indels	0;	Gaps	0;

CC 10 ERVTKILVDRUGVDEADVKLEASFKEDLGADSLDVWELVMELEDFDMISDEBAKAT 69
 CC |||||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 CC 5 ERVKKLVVEQLKEEVKPEASFVEDLGADSLDVWELVMALEEFDEIPDEEAKITT 64
 CC |:||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 70 VGDAVNTIQNQQ 81
 DB 65 VQSAYDIVQNNQ 76
 CC |:||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 CC Sequence 76 AA:

RESULT 6

ABU30165	standard; protein;	76 AA.
AC	ABU30165;	
XX	19-JUN-2003 (first entry)	
DE	Protein encoded by Prokaryotic essential gene #15592.	
XX	Antisense; prokaryotic essential gene; cell proliferation; drug design.	
XX	Haemophilus influenzae.	
PN	WO200277183-A2.	
XX	03-OCT-2002.	
PD		
XX		
PF	21-MAR-2002; 2002WO-US009107.	
XX	21-MAR-2001; 2001US-00815242.	
PR	06-SEP-2001; 2001US-00948993.	

Query Match

ABU30165	standard; protein;	76 AA.
AC	ABU30165;	
XX	19-JUN-2003 (first entry)	
DE	Protein encoded by Prokaryotic essential gene #15592.	
XX	Antisense; prokaryotic essential gene; cell proliferation; drug design.	
XX	Haemophilus influenzae.	
PN	WO200277183-A2.	
XX	03-OCT-2002.	
PD		
XX		
PF	21-MAR-2002; 2002WO-US009107.	
XX	21-MAR-2001; 2001US-00815242.	
PR	06-SEP-2001; 2001US-00948993.	

PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR N-PSDB; ACN34035.

XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 58089; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX Sequence 76 AA:

Query Match	64.0%	Score	254;	DB	6;	Length	76;
Best Local Similarity	72.2%	Pred.	No.	1.4e-20;	Mismatches	52;	Conservative
Matches	8;	Mismatches	12;	Indels	0;	Gaps	0;

CC 10 ERVTKILVDRUGVDEADVKLEASFKEDLGADSLDVWELVMELEDFDMISDEBAKAT 69
 CC |||||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 CC 5 ERVKKLVVEQLKEEVKPEASFVEDLGADSLDVWELVMALEEFDEIPDEEAKITT 64
 CC |:||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 70 VGDAVNTIQNQQ 81
 DB 65 VQSAYDIVQNNQ 76
 CC |:||:|||:|||:|||:|||:|||:|||:|||:|||:
 CC Sequence 76 AA:

RESULT 7

ABU39519	standard; protein;	76 AA.
AC	ABU39519;	
XX	19-JUN-2003 (first entry)	

Query Match

ABU39519	standard; protein;	76 AA.
AC	ABU39519;	
XX	19-JUN-2003 (first entry)	

DE Protein encoded by Prokaryotic essential gene #25046.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Pasteurella multocida.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PR 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-0094893.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW, Xu HH;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA,
 XX
 DR WPI; 2003-029926/02.
 XX
 PS N-PSDB; ACA43389.

XX
 CC New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for rational drug discovery programs.
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 67443; 176pp; English.

XX
 CC The invention relates to an isolated nucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:
 (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies on a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolat candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://ftpt.wipo.int/pub/published_pct_sequences](http://ftpt.wipo.int/pub/published_pct_sequences)
 XX
 SQ Sequence 76 AA;

Query Match 62.7%; Score 249; DB 6; Length 76;
 Best Local Similarity 70.8%; Pred. No. 5.2e-20; Mismatches 51; Conservative 9; Indels 0; Gaps 0;

OY 10 ERVKIIVDUGVDAVYKAEASFKEGDIGADSLDVYLNLNELEBDFMMEISDEDAEKAT 69
 5 ERVKIIVDUGVDAVYKAEASFKEGDIGADSLDVYLNLNELEBDFMMEISDEDAEKAT 64

Db

Qy	70	VGDAVNYIQNQQ	81
	65	VQSAIDYVONQQ	76
RESULT	8		
ABU49449			
ID	ABU49449	standard; protein;	110 AA.
XX			
AC	ABU49449;		
XX			
DT	19-JUN-2003	(first entry)	
XX			
DE	Protein encoded by Prokaryotic essential gene #34976.		
XX			
KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.		
XX			
OS	Vibrio cholerae.		
XX			
PN	W0200277183-A2.		
XX			
PD	03-OCT-2002.		
XX			
PR	21-MAR-2002; 2002WO-US009107.		
XX			
PR	21-MAR-2001; 2001US-00815242.		
PR	06-SEP-2001; 2001US-0094893.		
PR	25-OCT-2001; 2001US-0342923P.		
PR	08-FEB-2002; 2002US-00072851.		
PR	06-MAR-2002; 2002US-0362699P.		
XX			
XX			
PT	WPI; 2003-029926/02.		
XX			
PS	Claim 25; SEQ ID NO 77373; 176pp; English.		
XX			
CC	New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for rational drug discovery programs.		
CC	PT isolate candidate molecules for rational drug discovery programs.		
CC	XX		
CC	DR		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
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CC	WPI; 2003-029926/02.		
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CC	WPI; 2003-029926/02.		
CC	XX		
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CC	WPI; 2003-029926/02.		
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CC	WPI; 2003-029926/02.		
CC	XX		
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CC	WPI; 2003-029926/02.		
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CC	XX		
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CC	WPI; 2003-029926/02.		
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CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
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CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
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CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
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CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
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CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
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CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		
CC	XX		
CC	PS		
CC	XX		
CC	PT		
CC	WPI; 2003-029926/02.		

CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patient did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 110 AA;

Query Match 60.2%; Score 239; DB 6; Length 110;
 Best Local Similarity 72.1%; Pred. No. 1.1e-18;
 Matches 49; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 10 ERVTKITIVDRGVDADVKLASFKEPDGLGASLDLVLMVLEDEDFMEISDEDARKIAT 69
 38 ERVKKLTIVEQIGVDEAEVKNNSFVEDLGADSDTVELVMALBEERDTBIPDEEAKITT 97

QY 70 VGDAVNVI 77
 98 VQAQDLYV 105

SQ

RESULT 9

ABU43867

ID ABU43867 standard; protein; 77 AA.

AC ABU43867;

XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #29394.

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS *Staphylococcus haemolyticus*.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

PP 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00949993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA47737.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 7191; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 the 6213 antisense sequences given in the specification where expression
 of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
 encoding a polypeptide whose expression is inhibited by the antisense
 nucleic acid; (2) a host cell containing the vector; (3) an isolated

polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 proliferation or the activity of a gene in an operon required for
 proliferation; (7) identifying a compound that influences the activity of
 the gene product or that has an activity against a biological pathway
 required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids required
 CC for identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 drug discovery programs, or for screening homologous nucleic acids
 required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

SQ

RESULT 10

ABU42995

ID ABU42995 standard; protein; 77 AA.

AC ABU42995;

XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #28522.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS *Staphylococcus epidermidis*.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PR 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00949993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA46865.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 70919; 1766pp; English.

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